

FIGURE 1B

FIGURE 1A

Figure 2

|→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←|→FLEX
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTACCAAATGTGCCCTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCGCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGGTGCCTGGAGCTGCAGTGTGAGCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

FLEX←|
A T A P T A P
0526 GCCACAGCCCCGACAGCCCCG 0546

Figure 3

→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGGCTGGCGCCAGCCTGGAGCCCAACAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→FLEX
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCTGCTGGGTCCAAGATGCAAGGCTTGTCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTACCAAATGTGCTTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCTCTCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGTGGCTGGAGTGCAGTGTGAGCCGACTCCTCAACCTGCCACCCCATGGAGTCCCCGGCCCTGGAG 0525

FLEX←→hinge hinge←→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGAGCCCAATCTTGTGACAAAACCTCACACATGCCCAACCGTGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGAGCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGTGGACGTGAGCCAGAACCTGAGGTCAAGTTCAACTGGTACGTGGAGCGGCTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGGTGGTCTGCGTCTCACCGTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAG 0900

CH2←→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTGAGCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGC 1050

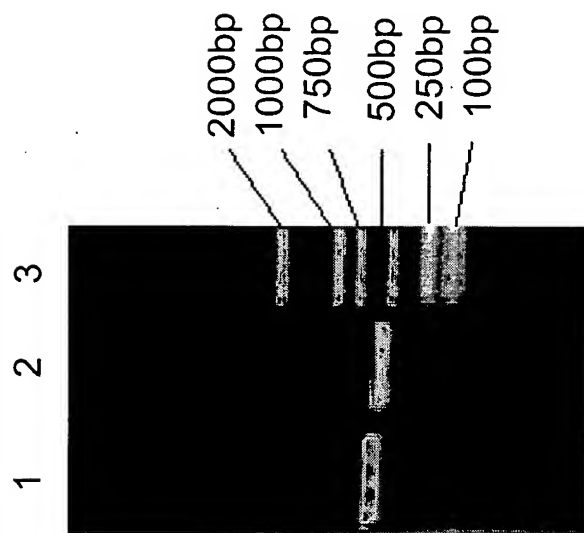
N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGCGAGCCGAGAACAACTACAAGACACGCTCCCGTGGTGGACTCCGACGGCTCCTTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1200

CH3←|
N H Y T Q K S L S L S P G K
1201 AACCACTACAGCAGAAGAGCCTCTCCCTGTCTCCCGTAAA 1242

Figure 4

G G G G S G G G S G G G S
GGCGGTGGAGGCTCTGGTGGAGGCGGTTTCAGGAGGCGGTGGATCT



Lane 1: mSM5-1 heavy chain variable region
Lane 2: mSM5-1 light chain variable region
Lane 3: DL2000 DNA Marker

FIGURE 5

Figure 6

[illegible]

Figure 7

0001 ATCATCACCAGAACAGCTTACGAGCAGACCGCCAGACAGCTCACAGGGATCAAGCTTGCCGCCACCATGGAATCA 0075
 Q T Q V F L S L L L W V S G T C G N I M M T Q S P
 0076 CAGACTCAGGTCCTCTCTCCCTGCTGCTCTGGGTATCTGGTACCTGTGGGAACATTATGATGACACAGTCGCCA 0150
 S S L A V S A G E K V T M S C K S S Q S V L Y S S
 0151 TCATCTCTGGCTGTGTCTGTCAGGAGAAAAAGGTCATATGAGCTGTAAGTCCAGTCAAAGTGTTTATACAGTTCA 0225
 N Q K N Y L A W Y Q Q K P G Q S P K L L I Y W A S
 0226 AATCAGAAGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATCTACTGGGCATCC 0300
 T R E S G V P D R F T G S G S G T D F T L T I S S
 0301 ACTAGGGAATCTGGTGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTTACTCTTACCATCAGCAGT 0375
 V Q A E A D L A V Y Y C H Q Y F S S Y T F G G G T K
 0376 GTACAGCTGAAGACTGGCAGTTTATTACTGTGTCATCAATATTCTCTCATACAGTTCGGAGGGGGGACCAAG 0450
 V_L ← |
 L E I K R
 0451 CTGGAATAAAAGCGG 0465

Figure 8

→SP SP←→VH
M E W S W I F L F L L S G T A G V H S E V
0001 ATCGCCGCCACCATGGAATGGAGTTGGATATTTCTCTTTCTCCTGTGAGGAAGTGCAGGTGTCCACTCTGAGGTC 0075
Q L Q Q S G P E L V K P G A S V K M S C K A S G Y
0076 CAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGTCTGCAAGGCTTCTGGATAC 0150
T F T S Y V M H W V K Q K P G Q G L D W I G Y I V
0151 ACATTCACTAGCTATGTTATGCACTGGGTGAAGCAGAAGCCTGGGCAGGGCCTTGACTGGATTGGATATATTGTT 0225
P Y N D G T K Y N E K F K G K A T L T S D K S S S
0226 CCTTACAATGATGGCACTAAGTACAATGAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGC 0300
T A Y M E L S R L T S E D S A V Y Y C V Y G S R Y
0301 ACAGCCTACATGGAGCTCAGCAGACTGACCTCTGAGGACTCTGCGGTCTATTATTGTGTCTACGGTAGTAGGTAC 0375
VH←→CH
D W Y L D V W G A G T T V T V S S A S T K G P S V
0376 GACTGGTATTTAGATGTCTGGGGCGCAGGGACCAAGGTACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGGAACTCAGGCGCCTGACCAGCGCGCTGCACACCTTCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCTGTGGAAGCAGGCTCAGCGCTCCTGCGCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCCGTCTGCTCTTCACCCGGAGCCTCTGCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAAECAGGCGCTGCACACAAAGGGCAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCCTGACCTAAGCCCCACCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAATCTTGTA 1125
K T H T C P P C P
1126 CAAACTCACACATGCCACCGTGCCAGGTAAGCCAGCCAGGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCTGCATCCAGGGACAGGCCCCAGCCGGTGTGACACGTCCACCTCCATCTCTTCCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAGCCAAAGGTGGGACCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCTTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGAGAGAACAACTACAAGACCAAGCCCTCCCGTGTCTGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1951 CCGACGGCTCTTCTCTCTCTACAGCAAGCTACCGTGGAACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 2025
S V M H E A L H N H Y T Q K S L S L S P G K STOP
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGTAAATGA 2021

Figure 9

0001 ATCATCACCAGAACAGCTTACGAGCAGACCGCCAGACAGCTCACAGGGATCAAGCTTGCCGCCACCATGGAATCA 0075
M E S
SP→
0076 Q T Q V F L S L L L W V S G T C G N I M M T Q S P
SP←→V_L
0151 CAGACTCAGGTCTTCCTCTCCCTGCTGCTCTGGGTATCTGGTACCTGTGGGAACATTATGATGACACAGTCGCCA 0150
S S L A V S A G E K V T M S C K S S Q S V L Y S S
0151 TCATCTCTGGCTGTGTCTGCAGGAGAAAAGTCACTATGAGCTGTAAGTCCAGTCAAAGTGTTTATACAGTTCA 0225
N Q K N Y L A W Y Q Q K P G Q S P K L L I Y W A S
0226 AATCAGAAGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAACTGCTGATCTACTGGGCATCC 0300
T R E S G V P D R F T G S G S G T D F T L T I S S
0301 ACTAGGGAATCTGGTGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTCTACTCTTACCATCAGCAGT 0375
V Q A E D L A V Y Y C H Q Y F S S Y T F G G G T K
0376 GTACAAGCTGAAGACCTGGCAGTTTATTACTGTCTCATCAATATTTCTCCTCATACAGTTCGGAGGGGGACCAAG 0450
V_L←→C_L
L E I K R T V A A P S V F I F P P S D E Q L K S G
0451 CTGGAATAAAGCGGACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA 0525
T A S V V C L L N N F Y P R E A K V Q W K V D N A
0526 ACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCC 0600
L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0601 CTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACC 0675
L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0676 CTGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG 0750
P V T K S F N R G E C Stop
0751 CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG 0786

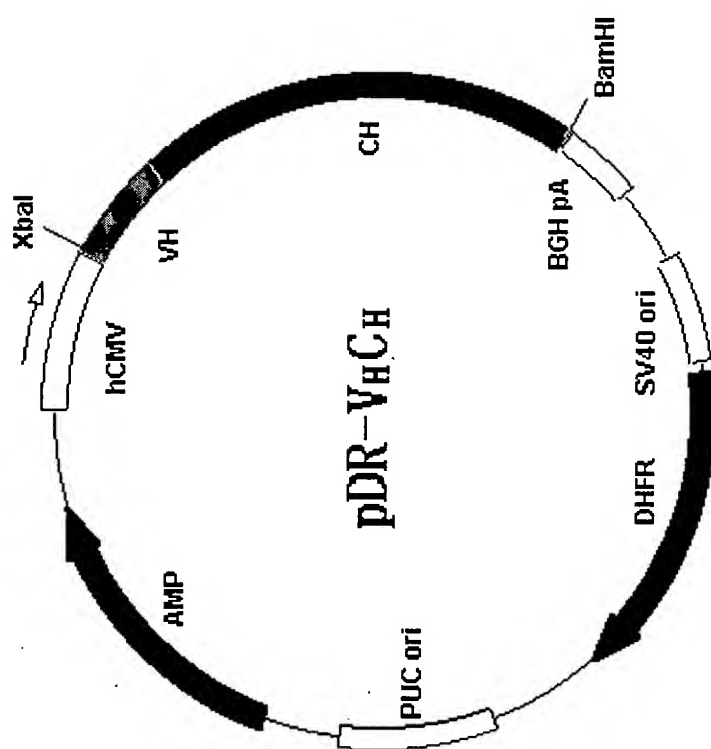


Figure 10

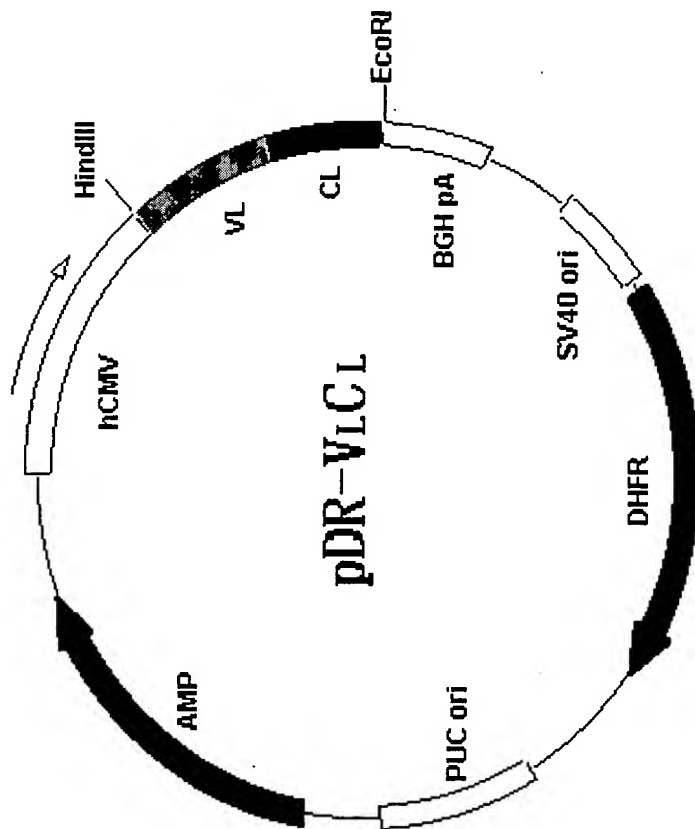


Figure 11

Figure 12

	→SP		SP← →VH
	M D W V W T L L F L L S V T A G V H S Q V		
0001	AGAGCCGCCACCATTGGGTGGTGACCTTGTCTATTCTGTGTGCAGTAATCGAGGTTGCCACTCCCAGGTG	0075	
	Q L V Q S G G G V V Q P G R S L R L S C K A S G Y		
0076	CAGCTGGTGCAGTCTGCGGTGGAGTGGTCCAGCCCCGGCCGAGCCTGAGGCTGTCTGCAAGGCATCTGGCTAC	0150	
	T F T S Y V M H W V R Q A P G K G L E W I G Y I V		
0151	ACCTTCACCAGCTACGTGATGACATGGGTGCGCCAAGCCCCGGAAAGGGCCTCGAATGGATTGGCTACATTGTG	0225	
	P Y N D G T K Y N E K F K G R F T I S S D K S K S		
0226	CCTTATAATGACGGTACTAAGTACAATGAAAAGTTCAAGGGGAGATTTACAATATCAAGTGACAAGAGCAAAGTCA	0300	
	T A F L Q M D S L R P E D T A V Y Y C A R G S R Y		
0301	ACCGCATTCCTCCAAATGGACAGCTTGCCTCCAGAGGACACCGCCGTATACTATTGTGTGCGCGGACCGCTTAC	0375	
			VH←
	D W Y L D Y W G Q G T P V T V S S z		
0376	GACTGTGACTTGGACTACTGGGGCCAAGGCACTCCAGTCACCGTCTCCTCT	0426	

Figure 13

```

                                |→SP
                                M D F Q V
0001 GAGCATTACGGGCATACCTCATCACCATCCCAGGATATCTCTAGAAAGCTTGCCGCCACCATGGATTTCCTCAAGTG 0075

                                SP←|→VL
      Q I F S F L L I S A S V I M S R G N I M M T Q S P
0076 CAGATTTCAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGAAACATCATGATGACTCAGAGCCCA 0150

      S S L S A S V G D R V T I T C K S S Q S V L Y S S
0151 TCCAGCTTGAGCGCATCAGTAGGCGACCGCGTAACGATCACTTGCAAATCCTCTCAGTCAGTATTGTACTCCAGC 0225

      N Q K N Y L A W Y Q Q T P G K A P K L L I Y W A S
0226 AACCGAAGAACTACTCTGGCCGGATATCAGCAGACTCCCGGCAAAGCCCCAAAGTTGTCTGATTATTGGGCCTCC 0300

      T R E S G V P S R F S G S G S G T D Y T F T I S S
0301 ACGCGCGAGTCTGGCGTGCCATCACGCTTTAGCGGCAGCGGGTCCGGTACAGATTACAGCTTTACCATTAGCAGT 0375

      L Q P E D I A T Y Y C H Q Y F S S Y T F G Q G T K
0376 CTGCAGCCTGAGGACATAGCCACCTACTACTGTCCAGTACTTTAGTTCCTACACTTTTGGCCAGGGAACATAAA 0450

      VL←|
      L Q I T R .
0451 CTGCAGATTACTCGA 0465

```

Figure 14

→SP SP←|→VH
M D W V W T L L F L L S V T A G V H S Q V
0001 AGAGCCGCCACCATGGATTGGGTGTGGACCTTGCTATTCTGTGTGTCAGTAAGTGCAGGTGTCCACTCCCAGGTG 0075
Q L V Q S G G G V V Q P G R S L R L S C K A S G Y
0076 CAGCTGGTGCAGTCTGGCGGTGGAGTGGTCCAGCCCGGCCGAGCCTGAGGCTGTCTCTGCAAGGCATCTGGCTAC 0150
T F T S Y V M H W V R Q A P G K G L E W I G Y I V
0151 ACCTTCACAGCTACGTGATGACATGGGTGCGCAAGCCCCGGAAGGGCCTCGAATGGATTGGCTACATTGTG 0225
P Y N D G T K Y N E K F K G R F T T I S S D K S K S
0226 CCTTATAATGACGGTACTAAGTACAATGAAAAGTTCAAGGGCAGATTACAATATCAAGTGACAAGAGCAAGTCA 0300
T A F L Q M D S L R P E D T A V Y Y C A R G S R Y
0301 ACCGCATTCTCCAAATGGACAGCTTTCGTCCAGAGGACACCGCGGTATACTATTGTGTGCGCGGCGAGCCGTAC 0375
VH←|→CH
D W Y L D Y W G Q G T P V T V S S A S T K G P S V
0376 GACTGGTACTTGGACTACTGGGGCCCAAGGCACTCCAGTCACCGTCTCCTCTGTAGCACCAAGGGCCCATCGGTG 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCCCTGGCACCCTCTCCAGAGCACTCTGGGGGCGACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGGAACCTCAGGCGCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCAAGCCCAAGCAACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCCTGCTGGAAGCAGGCTCAGCGCTCCTGCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCCGTCTGCTCTTCAACCGGAGCCTCTGCCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCGAGCACAGGCTAGGTGCCCTAACCCAGGCGCTGCACACAAAGGGGCGAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCGTGACCTAAGCCACCCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGTCCGACACCTTCTCTCTCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAATCTGTGA 1125
K T H T C P P C P
1126 CAAACTCACACATGCCACCGTGCCAGGTAAGCCAGCCAGGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCTGCATCCAGGGACAGGCCCCAGCGGGTGCTGACAGTCCACCTCCATCTCTTCTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAGGACACCCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGACGCGG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGTCTCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACAACTACAAGACCACGCCCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
S V M H E A L H N H Y T Q K S L S L S P G K STOP
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGTAAATGA 2021

Figure 15

0001 GAGCATTACCGCCATACTCATCACCATCCCAGSATATCTCTAGAAAGCTTGCCGCCACCATGGATTTTCAAGTG 0075
M D F Q V
|→SP
SP←|→V_L
Q I F S F L L I S A S V I M S R G N I M M T Q S P
0076 CAGATTTTCAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGAAACATCATGATGACTCAGAGCCCA 0150
S S L S A S V G D R V T I T C K S S Q S V L Y S S
0151 TCCAGCTTGAGCGCATCAGTAGGCGACCGCGTAACGATCACTTGCAAATCCTCTCAGTCAGTATTGTACTCCAGC 0225
N Q K N Y L A W Y Q Q T P G K A P K L L I Y W A S
0226 AACCAGAAGAACTACCTGGCCGATATCAGCAGACTCCCGGCAAAGCCCCAAAGTTGCTGATTTATTGGGCCTCC 0300
T R E S G V P S R F S G S G S G T D Y T F T I S S
0301 ACGCGCGAGTCTGGCGTGCCATCACGCTTTAGCGGCAGCGGGTCCGGTACAGATTACACGTTTACCATTAGCAGT 0375
L Q P E D I A T Y Y C H Q Y F S S Y T F G Q G T K
0376 CTGCAGCCTGAGGACATAGCCACCTACTACTGTCAACAGTACTTTAGTTCCTACACTTTTGCCAGGGAACATAA 0450
V_L←|→C_L
L Q I T R T V A A P S V F I F P P S D E Q L K S G
0451 CTGCAGATTACTCGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA 0525
T A S V V C L L N N F Y P R E A K V Q W K V D N A
0526 ACTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCC 0600
L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0601 CTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACC 0675
L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0676 CTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG 0750
P V T K S F N R G E C Stop
0751 CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGITAG 0786

Figure 16A

→SP SP←→VH
M D W V W T L L F L L S V T A G V H S Q V
0001 AGAGCCGCCACCATGGATTGGGTGTGGACCTTGCTATTCTGTGTGTCAGTAACTGCAGGTGTCCACTCCCAGGTG 0075
Q L V Q S G G G V V Q P G R S L R L S C K A S G Y
0076 CAGCTGGTGCACTCTGGCGGTGGAGTGGTCCAGCCCCGGCCGACGCTGAGGCTGTCTGCAAGGCATCTGGCTAC 0150
T F T S Y V M H W V R Q A P G K G L E W I G Y I V
0151 ACCTTCACCAGCTACGTGATGACATGGGTGCGCCAAGCCCCGAAAGGGCCTCGAATGGATTGGCTACATTGTG 0225
P Y N D G T K Y N E K F K G R F T I S S D K S K S
0226 CCTTATAATGACGGTACTAAGTACAATGAAAAGTTCAAGGGCAGATTTACAATATCAAGTGACAAGAGCAAGTCA 0300
T A F L Q M D S L R P E D T A V Y Y C A R G S R Y
0301 ACCGCATTCTCCAAATGGACAGCTTGGTCCAGAGGACACCGCGTATATACTATTGTGTGCGCGGACCGCTTAC 0375
VH←→CH
D W Y L D Y W G Q G T P V T V S S A S T K G P S V
0376 GACTGGTACTTGGACTACTGGGGCCAAGGCACTCCAGTCACCGTCTCCTCTGCTAGCACCAAGGGCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTACCGTGTCTTGGAACTCAGGCGCCCTGACAGCGCGGTGCACACCTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCCTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCCAGCAACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGT 0750
0751 TCTGCTGGAAGCAGGCTCAGCGCTCTGCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCCGTCTGCTCTTCACCCGGAGCCTCTGCCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCGCTGCACACAAAGGGGAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCTGACCTAAGCCCCACCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCCAGATTCCAGTAACTCCCAATCTTCTCTCTGAGAGCCCAATCTTGTGA 1125
K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCAGGTAAAGCCAGCCAGGCGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCTGCATCCAGGGACAGGCCCCAGCGGGTGTGACACGTCCACCTCCATCTCTCTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGACGTGAGCCAGAACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGCAAAGCCGCGGAGGAGCAGTACAACAGCAGCTACCGGTGGTCTGCGTCTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCAAAGGTGGGACCCGTGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CGACCTCTGCGCTGAGAGTGACGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCAAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCCATCCGGGATGAGCTGACCAAGAACAGGTGACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATGCGCGTGGAGTGGGAGAGCAATGGGACGCGGAGAACAACTACAAGACACGCTCCCGTGTCTGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGAGGGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
CH←→FLex
S V M H E A L H N H Y T Q K S L S L S P G K T Q D
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGGTAAACCCAGG 2025

C S F Q H S P I S S D F A V K I R E L S D Y L L Q
2026 ACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100
D Y P V T V A S N L Q D E E L C G G L W R L V L A
2101 AAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGG 2175
Q R W M E R L K T V A G S K M Q G L L E R V N T E
2176 CACAGCGCTGGATGGAGCGGCTCAAGACTGTCTGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGG 2250
I H F V T K C A F Q P P P S C L R F V Q T N I S R
2251 AGATACACTTTGTACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCC 2325
L L Q E T S E Q L V A L K P W I T R Q N F S R C L
2326 GCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCC 2400
E L Q C Q P D S S T L P P P W S P R P L E A T A P
2401 TGGAGCTGCAGTGTGAGCCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCCGGCCCTGGAGGCCACAGCCC 2475
T A P STOP
2476 CGACAGCCCCGTGA 2489

Figure 16B

Figure 17A

→SP SP←→VH
M D W V W T L L F L L S V T A G V H S Q V
0001 AGAGCCGCCACCATGGATTGGGTGTGGACCTTGCTATTCTGTGTGTCAGTAATGCAGGTGTCCACTCCCAGGTG 0075
Q L V Q S G G G V V Q P G R S L R L S C K A S G Y
0076 CAGCTGGTGAGTCTGGCGGTGGAGTGGTCCAGCCCGGCCGAGCCTGAGGCTGTCTGCAAGGCATCTGGCTAC 0150
T F T S Y V M H W V R Q A P G K G L E W I G Y I V
0151 ACCTTCACGAGCTACGTGATGACATGGGTGCGCAAGCCCGGAAAGGGCCTCGAATGGATTGGCTACATTGTG 0225
P Y N D G T K Y N E K F K G R F T I S S D K S K S
0226 CCTTATAATGACGGTACTAAGTACAATGAAAGTTCAAGGGCAGATTTACAATATCAAGTGACAAGAGCAAGTCA 0300
T A F L Q M D S L R P E D T A V Y Y C A R G S R Y
0301 ACCGCATTCTCCAAATGGACAGCTTGCGTCCAGAGGACACCGCGTATATACTATTGTGTGCGCGGACCGCTTAC 0375
VH←→CH
D W Y L D Y W G Q G T P V T V S S A S T K G P S V
0376 GACTGGTACTTGGACTACTGGGGCCAAAGGCACTCCAGTCACCGTCTCCTCTGCTAGCACCAAGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAAAGAGCACTCTGGGGGCACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGGAACTCAGGCGCCCTGACCAGCGCGTGACACACTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCAGCAACACCAAGGTGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCTGTGGAAGCAGGCTCAGCGCTCTGCGCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCGCTCTGCTCTTACCCGGAGCCTCTGCCCCCCTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAAAGGGGAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCCTGACCTAAGGCCACCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCCAGATTCCAGTAATCCCAATCTTCTCTCTGCAGAGCCCAATCTTGTGA 1125
K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCAGGTAAGCCAGCCAGGCTCGCCCTCCAGCTCAAGGCGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCTGCATCCAGGGACAGGCCCCAGCGGGTGCTGACAGTCCACCTCCATCTCTCTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGAGGCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCATCCGGGATGAGCTGACCAAGAACAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G O P E N N Y K T T P P V L D S
1801 GCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCGGAGAACTACAAGACCACGCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGACAAAGAGCAGGTGGCAGCAGGGGACGCTCTTCTCAT 1950
CH←→Linker
S V M H E A L H N H Y T Q K S L S L S P G K G G
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGTAAAGGCGGTG 2025

Linker←|→FLex
G S G G G G S G G G G S T Q D C S F Q H S P I S S
2026 GAGGCTCTGGTGGAGGCGGTTTCAGGAGGCGGTGGATCTACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCT 2100
D F A V K I R E L S D Y L L Q D Y P V T V A S N L
2101 CCGACTTCGCTGTCAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACC 2175
Q D E E L C G G L W R L V L A Q R W M E R L K T V
2176 TGCAGGACGAGGAGCTCTGCGGGGCCCTCTGGCGGCTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTG 2250
A G S K M Q G L L E R V N T E I H F V T K C A F Q
2251 TCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTACCAAATGTGCCTTTC 2325
P P P S C L R F V Q T N I S R L L Q E T S E Q L V
2326 AGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCTCCTGCAGGAGACCTCCGAGCAGCTGG 2400
A L K P W I T R Q N F S R C L E L Q C Q P D S S T
2401 TGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTGAGCCCGACTCCTCAA 2475
L P P P W S P R P L E A T A P T A P STOP
2476 CCCTGCCACCCCATGGAGTCCCCGGCCCTGGAGGCCACAGCCCCGACAGCCCCGTGA 2534

Figure 17B

Figure 18A

→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACCTATCTCCTCTGTGCTGTGCTGTGAGCTCGGGACTCAGT 0075

SP←→Flex
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTACCAAAATGTGCCTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCGCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAAGCTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGTGCCTGGAGCTGCAGTGTGAGCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

Flex←→hinge hinge←→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCCGTCGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGACACCTCATGATCTCCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGCTACCGGGTGGTCTGCGTCTCACCGTC 0825

L H Q . D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCGAGCCCCATCGAG 0900

CH2←→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTGAGCTGACCTGCTGGTCAAAGGCTTCTATCCCAGCGACATCGCGTGGAGTGGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGCAGCCGAGAACAACTACAAGACACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1200

CH3←→VH
N H Y T Q K S L S L S P G K Q V Q L V Q S G G G V
1201 AACCACTACAGCAGAAGAGCCTCTCCCTGTCTCCCGTAAACAGGTGCAGCTGGTGCAGTCTGGCGGTGGAGTG 1275

V Q P G R S L R L S C K A S G Y T F T S Y V M H W
1276 GTCCAGCCCGCGCAGCCTGAGGCTGTCTGCAAGGCATCTGGCTACACCTTACCAGCTACGTGATGACATGG 1350

V R Q A P G K G L E W I G Y I V P Y N D G T K Y N
1351 GTGCGCAAGCCCCGAAAGGGCCTCGAATGGATTGGCTACATTGTGCTTATAATGACGGTACTAAGTACAAT 1425

E K F K G R F T I S S D K S K S T A F L Q M D S L
1426 GAAAAGTTCAAGGGCAGATTACAATATCAAGTGACAAGCAAGTCAACCGATTCTCCAATGGACAGCTTG 1500

R P E D T A V Y Y C A R G S R Y D W Y L D Y W G Q
1501 CGTCCAGAGGACACCGCGTATACTATTGTGTGCGCGGACCGGTTACGACTGGTACTTGGACTACTGGGGCCAA 1575

VH←→Linker Linker←→V_L
G T P V T V S S G G G S G G G S G G G S N I
1576 GGCCTCCAGTCACCGTCTCCTCTGGCGGTGGAGGCTCTGGTGGAGGCGGTTCAGGAGGCGGTGGATCTAACATC 1650

M M T Q S P S S L S A S V G D R V T I T C K S S Q
1651 ATGATGACTCAGAGCCCATCCAGCTTGAGCGCATCAGTAGGCGACCGGTAACGATCACTTGCAAATCCTCTCAG 1725

S V L Y S S N Q K N Y L A W Y Q Q T P G K A P K L
1726 TCAGTATTGTACTCCAGCAACCAGAAGAACTACCTGGCCGATATCAGCAGACTCCCGGCAAAGCCCCAAGTTG 1800

L I Y W A S T R E S G V P S R F S G S G S G T D Y
1801 CTGATTTATTGGGCCTCCACGCGCAGTCTGGCGTGCCATCACGCTTTAGCGGCAGCGGGTCCGGTACAGATTAC 1875
T F T I S S L Q P E D I A T Y Y C H Q Y F S S Y T
1876 ACGTTTACCATTAGCAGTCTGCAGCCTGAGGACATAGCCACCTACTACTGTCCACAGTACTTTAGTTCCTACACT 1950
V_L←|
F G Q G T K L Q I T R STOP
1951 TTTGGCCAGGGAACATAAAGTCAGATTACTCGATGA 1986

Figure 18B

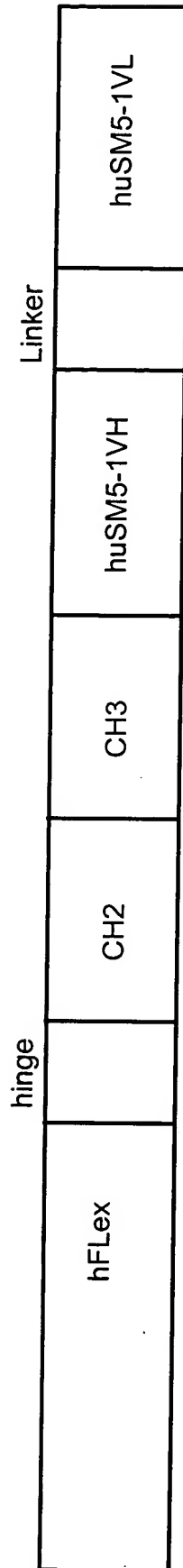


FIGURE 19

Figure 20A

SP→|→SP SP←|→VH
M E W S W I F L F L L S G T A G V H S E V
0001 CTGCGCCACCACATGGAATGGAGTTGGATATTCTCTTTCTCTCTGTCAGGAAGTCAGGTGTCCACTCTGAGGTC 0075
Q L Q Q S G P E L V K P G A S V K M S C K A S G Y
0076 CAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGTCTGCAAGGCTTCTGGATAC 0150
T F T S Y V M H W V K Q K P G Q G L D W I G Y I V
0151 ACATTCACTAGCTATGTTATGCACTGGGTGAAGCAGAAGCCTGGGCAGGGCCTTGACTGGATTGGATATATTGTT 0225
P Y N D G T K Y N E K F K G K A T L T S D K S S S
0226 CCTTACAATGATGGCACTAAGTACAATGAGAAGTTCAAAGGCAAGGCCACTGACTTCAGACAAATCCTCCAGC 0300
T A Y M E L S R L T S E D S A V Y Y C V Y G S R Y
0301 ACAGCCTACATGGAGCTCAGCAGACTGACCTCTGAGGACTCTGCGGTCTATTATTGTGTCTACGGTAGTAGGTAC 0375
VH←|→CH
D W Y L D V W G A G T T V T V S S A S T K G P S V
0376 GACTGGTATTTAGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGAACTCAGGCGCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCTGTGGAAGCAGGCTCAGCGCTCTGCTGGACGATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCCGTCTGCCTCTTCAACCGGAGCCTCTGCCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCTGACCTAAGCCCCACCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCTCCAGATTTCAGTAAGTCCCAATCTTCTCTCTGCAGAGCCCAATCTGTGA 1125
K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCAGGTAAGCCAGCCAGGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCTGCATCCAGGGACAGGCCCCAGCGGGTGTGACAGTCCACCTCCATCTCTTCTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGACGTGAGCCAGAACCTGAGGTCAAGTTCAAGTGTACGTGGACGGCG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCTGCGTCTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCGGTGGGGTGGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCAAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGCAACTACAAGACCAGCCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
S V M H E A L H N H Y T Q K S L S L S P G K T Q D
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGTAAACCCAGG 2025

C S F Q H S P I S S D F A V K I R E L S D Y L L Q
2026 ACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100

D Y P V T V A S N L Q D E E L C G G L W R L V L A
2101 AAGATTACCCAGTCACCGTGGCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGG 2175

Q R W M E R L K T V A G S K M Q G L L E R V N T E
2176 CACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGG 2250

I H F V T K C A F Q P P P S C L R F V Q T N I S R
2251 AGATACACTTGTACCAAATGTGCCTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCC 2325

L L Q E T S E Q L V A L K P W I T R Q N F S R C L
2326 GCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCC 2400

E L Q C Q P D S S T L P P P W S P R P L E A T A P
2401 TGGAGCTGCAGTGTACGCCCCGACTCCTCAACCTGCCACCCCATGGAGTCCCCGGGCCCTGGAGGCCACAGCCC 2475

T A P STOP
2476 CGACAGCCCCGTGA 2489

Figure 20B

Figure 21A

SP SP
M E W S W I F L F L L S G T A G V H S E V
0001 CTGCGCCACCATGGAATGGAGTTGGATATTTCTCTTCTCCTGTGAGAACTGCAGGTGTCCACTCTGAGGTC 0075
Q L Q Q S G P E L V K P G A S V K M S C K A S G Y
0076 CAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGTCTGCAAGGCTTCTGGATAC 0150
T F T S Y V M H W V K Q K P G Q G L D W I G Y I V
0151 ACATTCACTAGCTATGTTATGCACTGGGTGAAGCAGAAGCCTGGGCAGGGCCTTGACTGGATTGGATATATTGTT 0225
P Y N D G T K Y N E K F K G K A T L T S D K S S S
0226 CCTTACAATGATGGCACTAAGTACAATGAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGC 0300
T A Y M E L S R L T S E D S A V Y Y C V Y G S R Y
0301 ACAGCTACATGGAGCTCAGCAGACTGACCTCTGAGGACTCTGCGGTCTATTATTGTGTCTACGGTAGTAGGTAC 0375
VH CH
D W Y L D V W G A G T T V T V S S A S T K G P S V
0376 GACTGGTATTAGATGTCTGGGGCGCAGGGACCAAGGTACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGAACTCAGGCGCCTGACCAGCGCGTGCACACCTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCTGTGGAAGCAGGCTCAGCGCTCTGCTGGACGCATCCCGGCTATGCAGGCCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCCGTCTGCCTCTTCAACCGGAGCCTCTGCCCCCCTCACTATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCAGGCGCTGCACACAAAGGGGAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCGACCTAAGGCCACCCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCTCCAGATTCCAGTAACTCCCAATCTTCTCTCTGTCAGAGCCCAATCTTGTGA 1125
K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCCAAGTAAGCCAGCCAGGCGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCTAGAGTAGCTGCATCCAGGACAGGCCCCAGCGGGTGCTGACAGTCCACCTCCATCTTCTCTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCT 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGAGCTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGC 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAGCAAAGGTGGGACCGTGGGGTGCGAGGGCCACATGGACAGAGGCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCAAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCATCCGGGATGAGCTGACCAAGAACAGGTGACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G O P E N N Y K T T P P V L D S
1801 GCGACATCGCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACAACTACAAGACCAAGCCCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGAGCGTCTTCTCTCTCTACAGCAAGCTCAGGTGGACAAGAGCAGGTGGCAGCAGGGGACCTCTTCTCAT 1950
CH Linker
S V M H E A L H N H Y T Q K S L S L S P G K G G G
1951 GCTCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGTAAAGGCGGTG 2025

Linker←|→FLEX
G S G G G G S G G G G S T Q D C S F Q H S P I S S
2026 GAGGCTCTGGTGGAGGCGGTTGAGGAGGCGGTGGATCTACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCT 2100
D F A V K I R E L S D Y L L Q D Y P V T V A S N L
2101 CCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACC 2175
Q D E E L C G G L W R L V L A Q R W M E R L K T V
2176 TGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTG 2250
A G S K M Q G L L E R V N T E I H F V T K C A F Q
2251 TCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGGTGAACACGGAGATACACTTTGTACCAAATGTGCCTTTC 2325
P P P S C L R F V Q T N I S R L L Q E T S E Q L V
2326 AGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCTCCTGCAGGAGACCTCCGAGCAGCTGG 2400
A L K P W I T R Q N F S R C L E L Q C Q P D S S T
2401 TGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGTGCCTGGAGCTGCAGTGTGAGCCCGACTCCTCAA 2475
L P P P W S P R P L E A T A P T A P STOP
2476 CCCTGCCACCCCATGGAGTCCCGGCCCTGGAGGCCACAGCCCCGACAGCCCCGTGA 2534

Figure 21B

Figure 22A

→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACAACTATCTCCTCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→FLEX
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGAGCGGCTCAAGACTGTGCTGGGTCCAAGATGCAAGGCTTGTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTACCAATGTGCTTTTCAGCCCCCCCCAGCTGTCTGCTTCTGTCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCGCTCTGTCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGGTGCTGGAGCTGCAGTGTGAGCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCCGGCCCTGGAG 0525

FLEX←→HINGE hinge←→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGAGCCCAATCTTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCTCGGGGGACCGTCACTCTTCTCTCCCAAGGACACCTCATGATCTCCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACTATGCTGGTGGTGGAGCTGAGCCACGAAGACCTGAGGTCAAGTCAACTGGTACGTGGAGCGGTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGTGGTCTGCGTCTCACCCTG 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACCAGGACTGGCTGAATGGCAAGGAGTCAAGTGAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAG 0900

CH2←→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCAAAGCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCATCCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTGACCTGACCTGCTGCTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGCGAGCCGAGAACTACAAGACCGCTCCCGTGTGACTCGAGCGGCTCTTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGACAGAGCAGGTGGCAGCAGGGGAACGTCTCTCATGCTCCGTGATGATGAGGCTCTGCAC 1200

CH3←→VH
N H Y T Q K S L S L S P G K E V Q L Q Q S G P E L
1201 AACCACTACACGAGAGAGCCTCTCCTGTCTCCCGTAAAGAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTG 1275

V K P G A S V K M S C K A S G Y T F T S Y V M H W
1276 GTAAAGCCTGGGGCTTCAGTGAAGATGTCTGCAAGGCTTCTGGATACACATTCAGTAGCTATGTTATGCACTGG 1350

V K Q K P G Q G L D W I G Y I V P Y N D G T K Y N
1351 GTGAAGCAGAAGCCTGGGCAGGGCCTTGACTGGATTGGATATATGTTCCTTACAATGATGGCACTAAGTACAAT 1425

E K F K G K A T L T S D K S S S T A Y M E L S R L
1426 GAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCACAGCTACATGGAGCTCAGCAGACTG 1500

T S E D S A V Y Y C V Y G S R Y D W Y L D V W G A
1501 ACCTCTGAGGACTCTGCGGTCTATTATTGTGTCTACGGTAGTAGGTACGACTGGTATTAGATGTCTGGGGCGCA 1575

VH←→LINKER
G T T V T V S S G G G G S G G G G S G G G G S N I
1576 GGGACACGGTCACCGTCTCCTCAGGCGGTGGAGGCTCTGGTGGAGGCGGTTCCAGAGGCGGTGGATCTAACATT 1650

LINKER←→VL
M M T Q S P S S L A V S A G E K V T M S C K S S Q
1651 ATGATGACACAGTCGCCATCATCTCTGGCTGTGTCTGCAGGAGAAAAGGTCACTATGAGCTGTAAGTCCAGTCAA 1725

S V L Y S S N Q K N Y L A W Y Q Q K P G Q S P K L
1726 AGTGT TTTATACAGTTCAAATCAGAAGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG 1800

L I Y W A S T R E S G V P D R F T G S G S G T D F
1801 CTGATCTACTGGGCATCCACTAGGGAATCTGGTGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTT 1875

T L T I S S V Q A E D L A V Y Y C H Q Y F S S Y T
1876 ACTCTTACCATCAGCAGTGTACAAGCTGAAGACCTGGCAGTTTATTACTGTCATCAATATTTCTCCTCATACACG 1950

V_L ←|

F G G G T K L E I K R stop
1951 TTCGGAGGGGGACCAAGCTGGAAATAAAGCGGTGA 1986

Figure 22B

Figure 23

\rightarrow SP
M G F S R I F L F L L S V T T G V H S Q V Q L
0001 GCCACCATGGGATTCAGCAGGATCTTCTCTCCTCCTGTCACTAACTACAGGTGTCCATCCCAGGTACAACTA 0075
Q Q P G A E L V K P G A S V K M S C K A S G Y T F
0076 CAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCTCTGCAAGGCTTCTGGCTACACATTT 0150
T S Y N M H W V K Q T P G R G L E W I G A I Y P G
0151 ACCAGTTACAATATGCACTGGGTAAGCAGACACCTGGTCGGGGCCTGGAATGGATTGGAGCTATTATCCAGGA 0225
N G D T S Y N Q K F K G K A T L T A D K S S S T A
0226 AATGGTGATACTTCTCAATCAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCAGAGCC 0300
Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
0301 TACATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACGGCGGT 0375
D W Y F N V W G A G T T V T V S A
0376 GACTGGTACTTCAATGTCTGGGGCGCAGGGACCAGGTCACCGTCTCTGCA 0426
 $V_H \leftarrow$

Figure 24

[illegible]

Figure 25

SP ← | → V_H
M G F S R I F L F L L S V T T G V H S Q V Q L
0001 GCCACCATGGGATTTCAGCAGGATCTTTCTCTCTCTCTGTAGTAACACAGGTGTCCACTCCAGGTACAACCTA 0075

Q Q P G A E L V K P G A S V K M S C K A S G Y T F
0076 CAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCTGCAAGGCTTCTGGCTACACATTT 0150

T S Y N M H W V K Q T P G R G L E W I G A I Y P G
0151 ACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGTCGGGGCCTGGAATGGATTGGAGCTATTTATCCAGGA 0225

N G D T S Y N Q K F K G K A T L T A D K S S S T A
0226 AATGGTGATACTTCTACAATCAGAAGTTCAAGGGCAAGCCACTGACTGCAGACAAATCCTCCAGCAGAGCC 0300

Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
0301 TACATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACGGCGGT 0375

V_H ← | → C_H
D W Y F N V W G A G T T V T V S A A S T K G P S V
0376 GACTGGTACTTCAATGTCTGGGGCGCAGGGACACGGTCACCGTCTCTGCAGCTAGCACCAAGGGCCCATCGGTG 0450

F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525

P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGAACTCAGGCGCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600

S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675

N V N H K P S N T K V D K K V
0676 AACGTGAATCAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750

0751 TCTGTGGAAGCAGGCTCAGCGCTCTGCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825

0826 GGCCCGCTCTGCTCTTCAACCGGAGCCTCTGCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900

0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAG 0975

0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCTGACCTAAGCCCCCAAGGCCAAACTCTCCACTCCC 1050

E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCTCCAGATTCCAGTAACCTCCAATCTTCTCTCTGCAGAGCCAAATCTTGTA 1125

K T H T C P P C P
1126 CAAAACCTACACATGCCACCGTGCCAGGTAAGCCAGCCAGGCGCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200

A P
1201 CCTAGAGTAGCCTGCATCCAGGGACAGGCCCGGCTGCTGACACGTCCACCTCCATCTCTTCTCAGCAC 1275

E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 1350

E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTCAATGCGTGGTGGTGGACGTGAGCCAGAACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425

E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGCTACCGGTGGTCTGCGTCTCTCA 1500

V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAGGACTGGTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCAGCCCCCA 1575

E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGTGCGAGGGCCACATGGACAGAGCCGGCTCGGC 1650

G Q P R E P Q V Y T
1651 CCACCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725

L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCCATCCGGGATGAGCTGACCAAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800

D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATGCGCGTGGAGTGGGAGAGCAATGGGAGCGGAGAACAACTACAAGACCACGCTCCCGTGTGGACT 1875

D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGAGGCTCCTTCTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950

S V M H E A L H N H Y T Q K S L S L S P G K STOP
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGGTAATGA 2021

Figure 26

SP→|→V_L
M D F Q V Q I F S F L L I S A S V I M S R G Q I
0001 ACCATGGATTTCAGTGCAGATTTCAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAATT 0075
V L S Q S P A I L S A S P G E K V T M T C R A S S
0076 GTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTCAATGACTTGCAGGGCCAGCTCA 0150
S V S Y I H W F Q Q K P G S S P K P W I Y A T S N
0151 AGTGAAGTTACATCCACTGGTTCAGCAGAAGCCAGGATCCTCCCCAAACCCTGGATTATGCCACATCCAAC 0225
L A S G V P V R F S G S G S G T S Y S L T I S R V
0226 CTGGCTTCTGGAGTCCCTGTTTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGTAGAGTG 0300
E A E D A A T Y Y C Q Q W T S N P P T F G G G T K
0301 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTCCGGTGGTGGGACCAAG 0375
V_L←|→C_L
L E I K R T V A A P S V F I F P P S D E Q L K S G
0376 CTGGAGATCAAACGAACGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA 0450
T A S V V C L L N N F Y P R E A K V Q W K V D N A
0451 ACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCC 0525
L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0526 CTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACC 0600
L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0601 CTGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG 0675
P V T K S F N R G E C Stop
0676 CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG 0711

Figure 27A

I→SP SP←I→V_H
 M G F S R I F L F L L S V T T G V H S Q V Q L
 0001 GCCACCATGGGATTTCAGCAGGATCTTCTCTCTCTCTGTGCTAGTAACACAGGTGTCCACTCCCAGGTACAACCTA 0075
 Q Q P G A E L V K P G A S V K M S C K A S G Y T F
 0076 CAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACATTT 0150
 T S Y N M H W V K Q T P G R G L E W I G A I Y P G
 0151 ACCAGTTACAATATGCTCAGTGGGTAAGCAGACACCTGGTGGGGCTCGGAATGGATTGGAGCTATTATCCAGGA 0225
 N G D T S Y N Q K F K G K A T L T A D K S S S T A
 0226 AATGGTGATACCTCTACAATCAGAAGTTCAGGGGCAAGGCCACTGACTGCAGACAAATCCTCCAGCACAGCC 0300
 Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
 0301 TACATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACGGCGGT 0375
 D W Y F N V W G A G T T V T V S A A S T K G P S V
 0376 GACTGGTACTTCAATGTCTGGGCGCAGGGACCACGGTCAACGCTCTGTCAGCTAGCACCAAGGCCCATCGGTC 0450
 F P L A P S S K S T S G G T A A L G C L V K D Y F
 0451 TTCCCCCTGGCACCTCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525
 P E P V T V S W N S G A L T S G V H T F P A V L Q
 0526 CCCGAACCGGTGACGGTGTCTTGGAACTCAGGCGCCCTGACAGCGGGCTGCACACCTTCCCGGCTGCTCTACAG 0600
 S S G L Y S L S S V V T V P S S S L G T Q T Y I C
 0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
 N V N H K P S N T K V D K K V
 0676 AACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGCTGAGAGGGCAGCACAGGGAGGGAGGGTG 0750
 0751 CTGCTGGAAGCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
 0826 GGCCCCGTCTGCCTCTTACCGCGGAGCCTCTGCCCCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGCTTTTTC 0900
 0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTTAACCCAGGCGCTGCACACAAAGGGGCAGGTGCTGGGCTCAG 0975
 0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCTGACCTAAGCCACCCCAAAGGCCAAACTCTCCACTCCC 1050
 E P K S C D
 1051 TCAGTCTGGACACCTTCTCTCTCTCCAGATTCCAGTAACCTCCCAATCTTCTCTGTCAGAGCCCAATCTTGTA 1125
 K T H T C P P C P
 1126 CAAACTCACACATGCCACCGTGCCAGGTAAGCCAGCCAGGCGCTGCGCTCCAGCTCAAGGCGGGACAGGTG 1200
 A P
 1201 CCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTCTCTCAGCAC 1275
 E L L G G P S V F L F P P K P K D T L M I S R T P
 1276 CTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
 E V T C V V V D V S H E P E V K F N W Y V D D G V
 1351 CTGAGGTACATGCGTGGTGGTGACGTGAGCCAGGAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGCG 1425
 E V H N A K T K P R E E Q Y N S T Y R V V S V L T
 1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCTGCGTCTCA 1500
 V L H Q D W L N G K E Y K C K V S N K A L P A P I
 1501 CGGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
 E K T I S K A K
 1576 TCGAGAAAAACATCTCCAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGCTCGGC 1650
 G Q P R E P Q V Y T
 1651 CCACCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGCTCTACAGGGCAGCCCCGAGAACCAAGGTGTACA 1725
 L P P S R D E L T K N Q V S L T C L V K G F Y P S
 1726 CCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCTGGTCAAAGGCTTCTATCCCA 1800
 D I A V E W E S N G Q P E N N Y K T T P P V L D S
 1801 GCGACATCGCCGTGGAGTGGGAGAGCAATGGCGAGCGGAGAACCTACAAGACCACGCTCCCGTGTCTGGACT 1875
 D G S F F L Y S K L T V D K S R W Q Q G N V F S C
 1876 CCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCTAC 1950

CH \leftarrow →FLex
S V M H E A L H N H Y T Q K S L S L S P G K T Q D
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGGTAAAACCCAGG 2025

C S F Q H S P I S S D F A V K I R E L S D Y L L Q
2026 ACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100

D Y P V T V A S N L Q D E E L C G G L W R L V L A
2101 AAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGCTCTGGCGGCTGGTCTCTGG 2175

Q R W M E R L K T V A G S K M Q G L L E R V N T E
2176 CACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGG 2250

I H F V T K C A F Q P P P S C L R F V Q T N I S R
2251 AGATACACTTTGTACCAAATGTGCCTTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCC 2325

L L Q E T S E Q L V A L K P W I T R Q N F S R C L
2326 GCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCC 2400

E L Q C Q P D S S T L P P P W S P R P L E A T A P
2401 TGGAGCTGCAGTGTGAGCCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCGGCCCTGGAGGCCACAGCCC 2475

T A P STOP
2476 CGACAGCCCCGTGA 2489

Figure 27B

|→SP
 M G F S R I F L F L L S V T T G V H S Q V Q L
 0001 GCCACCATGGGATTGAGCAGGATCTTCTCTCTCTCTGTGAGTAACTACAGGTGCCACTCCAGGTACAACTA 0075
 Q Q P G A E L V K P G A S V K M S C K A S G Y T F
 0076 CAGCAGCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCTGCAAGGCTTCTGGCTACACATTT 0150
 T S Y N M H W V K Q T P G R G L E W I G A I Y P G
 0151 ACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGTGGGGCCTGGAATGGATTGGAGCTATTATCCAGGA 0225
 N G D T S Y N Q K F K G K A T L T A D K S S S T A
 0226 AATGGTGATACTTCTCAATCAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCTCCAGCAGACCC 0300
 Y M Q L S S L T S E D S A V Y Y C A R S T Y Y G G
 0301 TACATGCAGCTCAGCAGCTGACATCTGAAGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACGGCGGT 0375
 D W Y F N V W G A G T T V T V S A A S T K G P S V
 0376 GACTGGTACTTCAATGTCTGGGGCGCAGGGACCAAGGTACCGTCTCTGCAGCTAGACCAAGGGCCCATCGGT 0450
 F P L A P S S K S T S G G T A A L G C L V K D Y F
 0451 TTCCCTCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCAAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTC 0525
 P E P V T V S W N S G A L T S G V H T F P A V L Q
 0526 CCCGAACCGGTGACGGTGTCTTGGAACTCAGGCGCCCTGACAGCGGCTGCACACCTTCCGGCTGTCTCTACAG 0600
 S S G L Y S L S S V V T V P S S S L G T Q T Y I C
 0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
 N V N H K P S N T K V D K K V
 0676 AACGTGAATCACAGCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAAGGGCCAGCACAGGGAGGGAGGGT 0750
 0751 TCTGCTGGAAGCAGGCTCAGCGCTCTGCTCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
 0826 GGCCCGTCTGCTCTCTCTACCCGGAGCCTCTGCGCGCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
 0901 CAGGCTCTGGGCAGGCAAGGCTAGGTGCCCTAACCAGGCCCTGCACACAAAGGGGAGGTGTCTGGGCTCAG 0975
 0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCTGACCTAAGCCACCCCAAAGGCCAAATCTCCACTCCC 1050
 E P K S C D
 1051 TCAGCTCGGACACCTTCTCTCTCCAGATTCCAGTAACTCCCAATCTTCTCTGCGAGAGCCAAATCTGTGA 1125
 K T H T C P P C P
 1126 CAAAACCTCACATGCCCCCGTGCCAGGTAAGCCAGCCAGGCTCTGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
 A P
 1201 CCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCGGGTGCTGACAGCTCCACCTCCATCTCTTCTCTCAGCAC 1275
 E L L G G P S V F L F P P K P K D T L M I S R T P
 1276 CTGAATCTCTGGGGGACCGTCACTTCTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
 E V T C V V V D V S H E P E V K F N W Y V D D G V
 1351 CTGAGGTACATGCGTGGTGGAGCTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425
 E V H N A K T K P R E E G A G C A G T A C A A S T Y R V V S V L T
 1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCAGCTACCGGTGGTCTGGCTCTCT 1500
 V L H Q D W L N G K E Y K C K V S N K A L P A P I
 1501 CGTCTGCAACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCA 1575
 E K T I S K A K
 1576 TCGAGAAAACCATCTCCAAGGCCAAAGGTGGGACCCGTGGGGTGGCAGGGGCCATGGACAGAGGCGGGCTCGGC 1650
 G Q P R E P Q V Y T
 1651 CCACCTCTGCCCCTGAGAGTGACCGCTGTACCAACCTCTGTCTTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
 L P P S R D E L T K N Q V S L T C L V K G F Y P S
 1726 CCCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
 D I A V E W E S N G Q P E N N Y K T T P P V L D S
 1801 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACAACTACAAGACCAGCCCTCCCGTGTGGACT 1875
 D G S F F L Y S K L T V D K S R W Q Q G N V F S C
 1876 CCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
 CH←→Linker
 S V M H E A L H N H Y T Q K S L S L S P G K G G G
 1951 GCTCCGTGATGATGAGGCTCTGCACAACCACTACACGAGAAGAGCTCTCCCTGTCTCCCGGTAAAGGCGGTG 2025

Linker←|→FLEX

G S G G G G S G G G G S T Q D C S F Q H S P I S S
2026 GAGGCTCTGGTGGAGGCGGTTTCAGGAGGCGGTGGATCTACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCT 2100

D F A V K I R E L S D Y L L Q D Y P V T V A S N L
2101 CCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACC 2175

Q D E E L C G G L W R L V L A Q R W M E R L K T V
2176 TGCAGGACGAGGAGCTCTGCGGGGCTCTGGCGGCTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTG 2250

A G S K M Q G L L E R V N T E I H F V T K C A F Q
2251 TCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTACCAAATGTGCCTTTC 2325

P P P S C L R F V Q T N I S R L L Q E T S E Q L V
2326 AGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCTCTTGAGGAGACCTCCGAGCAGCTGG 2400

A L K P W I T R Q N F S R C L E L Q C Q P D S S T
2401 TGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGTGCCTGGAGCTGCAGTGTGAGCCCGACTCCTCAA 2475

L P P P W S P R P L E A T A P T A P STOP
2476 CCCTGCCACCCCATGGAGTCCCGGCCCTGGAGGCCACAGCCCGACAGCCCGTGA 2534

Figure 28B

Figure 29A

→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACAACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→Flex
G T Q D C S F Q H S P I S S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCAGCGCTGGATGGAGCGCTCAAGACTGTGCTGGTCCAAGATGCAAGGCTTGTCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTCAACAAATGTGCTTTTCAGCCCCCCCCAGCTGTCTTCTGCTTCTGCTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCGCTCTCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGTGCCTGGAGTGCAGTGTGAGCCGACTCCTCAACCTGCCACCCCATGGAGTCCCCGGCCCTGGAG 0525

Flex←→hinge hinge←→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGAGCCCAATCTTGTGACAAAACCTCACATGCCCCACCGTGGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGCGCTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGCTACCGGTGGTCTGCGTCTCACCGTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACGAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCGACCCCCATCGAG 0900

CH2←→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTCAGCCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGCGAGCCGAGAACAACTACAAGACACGCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1200

CH3←→VH
N H Y T Q K S L S L S P G K Q V Q L Q Q P G A E L
1201 AACCACTACAGCAGAAGAGCCTCTCCTGTCTCCCGTAAACAGGTACAACCTACAGCAGCCTGGGGCTGAGCTG 1275

V K P G A S V K M S C K A S G Y T F T S Y N M H W
1276 GTGAAGCCTGGGCGCTCAGTGAAGATGTCTGCAAGGCTTCTGGCTACACATTACAGTTACAATATGCACTGG 1350

V K Q T P G R G L E W I G A I Y P G N G D T S Y N
1351 GTAAAGCAGACACCTGGTGGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCTTACAAT 1425

Q K F K G K A T L T A D K S S S T A Y M Q L S S L
1426 CAGAAGTTCAAGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCTACATGCAGCTCAGCAGCCTG 1500

T S E D S A V Y Y C A R S T Y Y G G D W Y F N V W
1501 ACATCTGAAGACTCTGCGTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTCAATGTCTGG 1575

V_H←→Linker Linker←→
G A G T T V T V S A G G G G S G G G G S G G G G S
1576 GGCGCAGGACCAAGGTCAACGTCTCTGAGGCGGTGGAGGCTCTGGTGGAGCGGTTTCAAGAGGCGGTGGATCT 1650

→V_L
Q I V L S Q S P A I L S A S P G E K V T M T C R A
1651 CAAATTGTTCTCTCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTACAATGACTTGCAGGGCC 1725

S S S V S Y I H W F Q Q K P G S S P K P W I Y A T
1726 AGCTCAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGATCCTCCCCAAACCCTGGATTATGCCACA 1800

S N L A S G V P V R F S G S G S G T S Y S L T I S
1801 TCCAACCTGGCTTCTGGAGTCCCTGTTTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGT 1875

R V E A E D A A T Y Y C Q Q W T S N P P T F G G G
1876 AGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTCCGGTGGTGGG 1950
V_L ← |

T K L E I K R STOP
1951 ACCAAGCTGGAGATCAAACGATGA 1974

Figure 29B

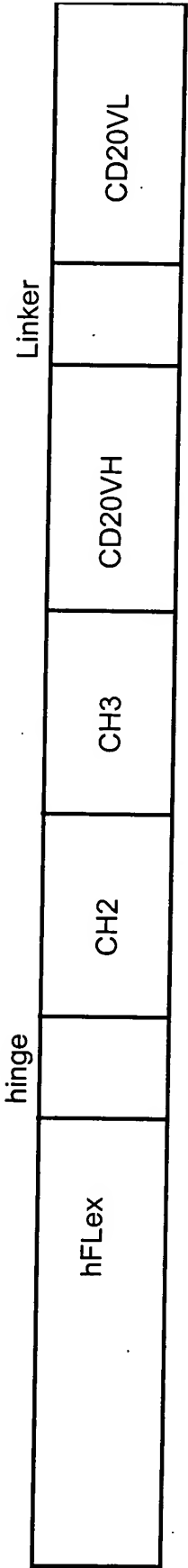


FIGURE 30

Figure 31

|→SP SP←|→VH
M D F Q V Q I F S F L L I S A S V I I S R G E V Q
0001 ATGGATTTTCAGGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATAATATCCAGAGGAGAGGTTTCAG 0075
L V E S G G G L V Q P G G S L R L S C A A S G F N
0076 CTGGTGGAGTCTGGCGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCTGTGCAGCTTCTGGCTTCAAC 0150
I K D T Y I H W V R Q A P G K G L E W V A R I Y P
0151 ATTAAGACACCTATATACACTGGGTGCGTCAGGCCCGGTAAGGGCCTGGAATGGGTGCAAGGATTTATCCT 0225
T N G Y T R Y A D S V K G R F T I S A D T S K N T
0226 ACGAATGGTTATACTAGATATGCCGATAGCGTCAAGGGCCGTTTCACTATAAGCGCAGACACATCCAAAACACA 0300
A Y L Q M N S L R A E D T A V Y Y C S R W G G D G
0301 GCCTACCTGCAGATGAACAGCCTGCGTGTGAGGACACTGCCGTCTATTATGTTCTAGATGGGGAGGGGACGGC 0375
VH←|
F Y A M D Y W G Q G T L V T V S S
0376 TTCTATGCTATGGACTACTGGGTCAAGGAACCTGGTCACCGTCTCCTCG 0426

Figure 32

|→SP SP←|→VL
M D F Q V Q I F S F L L I S A S V I I S R G D I Q
0001 ATGGATTTTCAGGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATAATATCCAGAGGAGACATCCAG 0075
M T Q S P S S L S A S V G D R V T I T C R A S Q D
0076 ATGACCCAGTCCCGAGCTCCCTGTCCGCCTCTGTGGGCGATAGGGTTACCATCACCTGCCGTGCCAGTCAGGAT 0150
V N T A V A W Y Q Q K P G K A P K L L I Y S A S F
0151 GTGAATACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCTCCGAAACTACTGATTTACTCGGCATCCTTC 0225
L Y S G V P S R F S G S R S G T D F T L T I S S L
0226 CTCTACTCTGGAGTCCCTTCTCGCTTCTCTGGCTCCAGATCTGGGACGGATTTCACCTCTGACCATCAGCAGTCTG 0300
Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K
0301 CAGCCGGAAGACTTCGCAACTTATTACTGTCAGCAACATTATACTACTCCTCCACGTTTCGGACAGGGTACCAAG 0375
VL←|
V E I K R
0376 GTGGAGATCAAACGT 0390

Figure 33

→SP SP←→VH
M D F Q V Q I F S F L L I S A S V I I S R G E V Q
0001 ATGGATTTCAGGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATAATATCCAGAGGAGGTTTCAG 0075
L V E S G G G L V Q P G G S L R L S C A A S G F N
0076 CTGGTGGAGTCTGGCGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCTGTGCAGCTTCTGGCTTCAAC 0150
I K D T Y I H W V R Q A P G K G L E W V A R I Y P
0151 ATTAAAGACACCTATATACACTGGGTGCGTCAGGCCCGGGTAAGGGCCTGGAATGGGTGCAAGGATTTATCCT 0225
T N G Y T R Y A D S V K G R F T I S A D T S K N T
0226 ACGAATGGTATAGTATAGCCGATAGCGTCAAGGGCGTTTCACTATAAGCGCAGACACATCCAAAAACACA 0300
A Y L Q M N S L R A E D T A V Y Y C S R W G G D G
0301 GCCTACCTGCAGATGAACAGCCTGCGTGTCTGAGGACACTGCCGTCTATTATTGTTCTAGATGGGGAGGGGACGGC 0375
VH←→CH
F Y A M D Y W G Q G T L V T V S S A S T K G P S V
0376 TTCTATGCTATGGACTACTGGGGTCAAGGAACCTGGTCACCGTCTCTCGGCTAGCACCAAGGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCGCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCAAGAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
TCTGTGGAAGCAGGCTCAGCGCTCCTGCGCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
GGCCCCGTCTGCTCTTCAACCGGAGCCCTCTGCCCCGCCCTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCGCTGCACACAAAGGGGAGGTGCTGGGCTCAG 0975
ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCTGACCTAAGCCACCCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGTCTCGACACCTTCTCTCTCCTCCAGATTCCAGTAACCTCCCAATCTTCTCTCTGCAGAGCCCAATCTTGTA 1125
K T H T C P P C P
1126 CAAAACCTCACATGCCCCACCGTGCCAGGTAAGCCAGCCAGGCGCTCGCCCTCCAGCTCAAGGGCGGACAGGTG 1200
A P
1201 CCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCGGGTGTGACACGTCCACCTCCATCTCTTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGACGTGAGCCAGAACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACAGGACTGGTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCGGTGGGCTGCGAGGGCCACATGGACAGAGGCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTGACGCTGACCTGCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATCGCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACAACTACAAGACCAGCCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
S V M H E A L H N H Y T Q K S L S L S P G K STOP
1951 GCTCCGTGATGCATGAGGCTCTGCACAAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGGTAATGA 2021

Figure 34

↳SP SP↳↳VL
M D F Q V Q I F S F L L I S A S V I I S R G D I Q
0001 ATGGATTTCAGGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATAATATCCAGAGGAGACATCCAG 0075
M T Q S P S S L S A S V G D R V T I T C R A S Q D
0076 ATGACCCAGTCCCCGAGCTCCCTGTCCGCCTCTGTGGGCGATAGGGTTACCATCACCTGCCGTGCCAGTCAGGAT 0150
V N T A V A W Y Q Q K P G K A P K L L I Y S A S F
0151 GTGAATACTGCTGTAGCCTGGTATCAACAGAAACAGGAAAAGCTCCGAACTACTGATTTACTCGGCATCCTTC 0225
L Y S G V P S R F S G S R S G T D F T L T I S S L
0226 CTCTACTCTGGAGTCCCTTCTCGCTTCTCTGGCTCCAGATCTGGGACGGATTTCACTCTGACCATCAGCAGTCTG 0300
Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K
0301 CAGCCGGAAGACTTCGCAACTTATTACTGTCAACATTATATACTACTCTCCACGTTCCGACAGGGTACCAAG 0375
VL↳↳CL
V E I K R T V A A P S V F I F P P S D E Q L K S G
0376 GTGGAGATCAAACGTACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA 0450
T A S V V C L L N N F Y P R E A K V Q W K V D N A
0451 ACTGCCTCTGTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCC 0525
L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
0526 CTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACC 0600
L T L S K A D Y E K H K V Y A C E V T H Q G L S S
0601 CTGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG 0675
P V T K S F N R G E C Stop
0676 CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAG 0711

Figure 35A

SP←|→VH
M D F Q V Q I F S F L L I S A S V I I S R G E V Q
0001 ATGGATTTCAGGTGCAGATTTCAGCTTCTGCTAATCAGTGCCTCAGTCATAATATCCAGAGGAGGTTTCAG 0075
L V E S G G G L V Q P G G S L R L S C A A S G F N
0076 CTGGTGGAGTCTGGCGGTGGCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCTGTGCAGCTTCTGGCTTCAAC 0150
I K D T Y I H W V R Q A P G K G L E W V A R I Y P
0151 ATTAAAGACACCTATATACACTGGGTGCGTCAGGCCCGGGTAAGGGCCTGGAATGGGTGCAAGGATTTATCCT 0225
T N G Y T R Y A D S V K G R F T I S A D T S K N T
0226 ACGAATGGTTATACTAGATATGCCGATAGCGTCAAGGGCCGTTTCACTATAAGCGCAGACACATCCAAAAACACA 0300
A Y L Q M N S L R A E D T A V Y Y C S R W G G D G
0301 GCCTACCTGCAGATGAACAGCCTGCGTGTGAGGACACTGCCGTCTATTATGTTCTAGATGGGAGGGGACGGC 0375
VH←|→CH
F Y A M D Y W G Q G T L V T V S S A S T K G P S V
0376 TTCTATGCTATGGACTACTGGGTCAAGGAACCTGGTCACCGTCTCCTCGGCTAGCACCAAGGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGTGTCTTGGAACTCAGGCGCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCAGCAACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
0751 TCTGCTGGAAGCAGGCTCAGCGCTCCTGCTGGACGCATCCCGGCTATGCAGCCCAGTCCAGGGCAGCAAGGCA 0825
0826 GGCCCCGTCTGCTCTTCAACCGGAGCCTCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
0901 CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAAAGGGCAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCTGACCTAAGCCCCACCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCCAGATTCCAGTAAGTCCCAATCTTCTCTCTGCGAGGCCCAATCTTGTA 1125
K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCCAAGTAAGCCAGCCAGGCCCTCGCCCTCCAGCTCAAGGCGGACAGGTG 1200
A P
1201 CCTAGATAGCTGCATCCAGGGACAGGCCCCAGCGGGTGTGACACGCTCCACCTCCATCTCTTCTCCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGGTGGTCTGCGTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCAGAGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCCCTCTGCGCTGAGAGTGACCGCTGTACCAACCTCTGTCTCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATGCGCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACAACTACAAGACCACGCTCCCGTGTCTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950

CH←|→FLEX

1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGTAAAACCCAGG 2025

2026 ACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGACTACCTGCTTC 2100

2101 AAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGCCTCTGGCGGCTGGTCTCTGG 2175

2176 CACAGCGCTGGATGGAGCGGCTCAAGACTGTGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGG 2250

2251 AGATACACTTTGTACCAAATGTGCCTTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCC 2325

2326 GCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCC 2400

2401 TGGAGCTGCAGTGTGAGCCCGACTCCTCAACCTGCCACCCCATGGAGTCCCGGCCCTGGAGGCCACAGCCC 2475

2476 CGACAGCCCCGTGA 2489

T A P STOP

Figure 35B

Figure 36A

SP<|>VH
M D F Q V Q I F S F L L I S A S V I I S R G E V Q
0001 ATGGATTTCAGGTGCAGATTTCAGCTTCTGCTAATCAGTGCCTCAGTCATAATATCCAGAGGAGGTTTCAG 0075
L V E S G G G L V Q P G G S L R L S C A A S G F N
0076 CTGGTGGAGTCTGGCGGTGGCTGGTGCAGCCAGGGGCTCACTCCGTTTGTCTGTGCAGCTTCTGGCTTCAAC 0150
I K D T Y I H W V R Q A P G K G L E W V A R I Y P
0151 ATTAAAGACACCTATATACACTGGGTGCGTCAGGCCCGGGTAAGGGCCTGGAATGGGTGCAAGGATTTCCTCT 0225
T N G Y T R Y A D S V K G R F T I S A D T S K N T
0226 ACGAATGGTTATACTAGATATGCCGATAGCGTCAAGGGCGGTTTCACTATAAGCGCAGACACATCCAAAAACACA 0300
A Y L Q M N S L R A E D T A V Y Y C S R W G G D G
0301 GCCTACCTGCAGATGAACAGCCTGCGTGTGAGGACACTGCCGTCTATTATTGTTCTAGATGGGGAGGGGACGGC 0375
VH<|>CH
F Y A M D Y W G Q G T L V T V S S A S T K G P S V
0376 TTCTATGCTATGGACTACTGGGTCAAGGAACCTGGTCACCGTCTCTCGGCTAGCACCAAGGGCCCATCGGTC 0450
F P L A P S S K S T S G G T A A L G C L V K D Y F
0451 TTCCCTCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTC 0525
P E P V T V S W N S G A L T S G V H T F P A V L Q
0526 CCCGAACCGGTGACGGTGTCTTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAG 0600
S S G L Y S L S S V V T V P S S S L G T Q T Y I C
0601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 0675
N V N H K P S N T K V D K K V
0676 AACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 0750
TCTGTGGAAGCAGGCTCAGCGCTCTGCTGCGTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCA 0825
GGCCCCGTCTGCTCTTACCCCGAGCCCTCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTC 0900
CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAG 0975
0976 ACCTGCCAAGAGCCATATCCGGGAGGACCTGCCCCGACCTAAGCCCCAACCCAAAGGCCAAACTCTCCACTCCC 1050
E P K S C D
1051 TCAGCTCGGACACCTTCTCTCTCTCCAGATTCCAGTAACCTCCCAATCTTCTCTCTGACAGAGCCCAATCTGTGA 1125
K T H T C P P C P
1126 CAAAACCTCACACATGCCACCGTGCCCAAGTAAGCCAGCCAGGCCCTCGCCCTCCAGCTCAAGGCGGGACAGGTG 1200
A P
1201 CCCTAGATAGCTGCATCCAGGGACAGGCCCCAGCCGGGTGCTGACAGCTCCACCTCCATCTCTTCTCAGCAC 1275
E L L G G P S V F L F P P K P K D T L M I S R T P
1276 CTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCC 1350
E V T C V V V D V S H E P E V K F N W Y V D D G V
1351 CTGAGGTCAATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGG 1425
E V H N A K T K P R E E Q Y N S T Y R V V S V L T
1426 TGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCTCA 1500
V L H Q D W L N G K E Y K C K V S N K A L P A P I
1501 CCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA 1575
E K T I S K A K
1576 TCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCGGTGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGC 1650
G Q P R E P Q V Y T
1651 CCACCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCTACAGGGCAGCCCCGAGAACCACAGGTGTACA 1725
L P P S R D E L T K N Q V S L T C L V K G F Y P S
1726 CCCTGCCCCCATCCCGGATGAGCTGACCAAGAAACAGGTGACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1800
D I A V E W E S N G Q P E N N Y K T T P P V L D S
1801 GCGACATGCGCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCTCCCGTGTGGACT 1875
D G S F F L Y S K L T V D K S R W Q Q G N V F S C
1876 CCGACGGCTCTTCTCTCTCTACAGCAAGCTCACCGTGACAAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT 1950
CH<|>Linker
S V M H E A L H N H Y T Q K S L S L S P G K G G
1951 GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCCGTAAAGGCGGTG 2025

Linker←|→FLEX

2026 G A G G C T C T G G T G G A G G C G G T T C A G G A G G C G G T G G A T C T A C C C A G G A C T G C T C C T T C C A A C A C A G C C C C A T C T C C T 2100

2101 D F A V K I R E L S D Y L L Q D Y P V T V A S N L
C C G A C T T C G C T G T C A A A A T C C G T G A G C T G T C T G A C T A C C T G C T T C A A G A T T A C C C A G T C A C C G T G G C C T C C A A C C 2175

2176 Q D E E L C G G L W R L V L A Q R W M E R L K T V
T G C A G G A C G A G G A G C T C T G C G G G G C C T C T G G C G G T G G T C C T G G C A C A G C G C T G G A T G G A G C G G C T C A A G A C T G 2250

2251 A G S K M Q G L L E R V N T E I H F V T K C A F Q
T C G C T G G G T C C A A G A T G C A A G G C T T G C T G G A G C G C T G A A C A C G G A G A T A C A C T T T G T C A C C A A A T G T G C C T T T C 2325

2326 P P P S C L R F V Q T N I S R L L Q E T S E Q L V
A G C C C C C C C C A G C T G T C T T C G C T T C G T C C A G A C C A A C A T C T C C C G C C T C C T G C A G G A G A C C T C C G A G C A G T G G 2400

2401 A L K P W I T R Q N F S R C L E L Q C Q P D S S T
T G G C G C T G A A G C C C T G G A T C A C T C G C C A G A A C T T C T C C C G G T G C C T G G A G C T G C A G T G T C A G C C C G A C T C T C A A 2475

2476 L P P P W S P R P L E A T A P T A P STOP
C C T G C C A C C C C A T G G A G T C C C C G G C C C T G G A G G C C A C A G C C C G A C A G C C C G T G A 2534

Figure 36B

Figure 37A

↳SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACACCTATCTCCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←|→FLEX
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCATCTCCTCCGACTTCGCTGTCAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACACGCTGGATGGAGCGCTCAAGACTGTGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTACCAAATGTGCCCTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGTGTCTGGAGTGCAGTGTAGCCCGACTCCTCAACCCCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

FLEX←|→hinge hinge←|→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGAGGCCCAAATCTTGTGACAAAACCTCACACATGCCACCCGTGCCAGCACCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGTACCGGGTGGTCTGCGTCTCACCCTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGTCTCCAACAAGCCCTCCAGCCCCCATCGAG 0900

CH2←|→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTGAGCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGCAGCCGAGAACAACTACAAGACCAGCCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGAACAAGAGCAGGTGGCAGCAGGGGAAGCTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1200

CH3←|→VH
N H Y T Q K S L S L S P G K E V Q L V E S G G G L
1201 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGTAAAGAGGTTCAAGTGGTGGAGTCTGGCGGTGGCCTG 1275

V Q P G G S L R L S C A A S G F N I K D T Y I H W
1276 GTGCAGCCAGGGGGCTCACTCCGTTTGTCTGTGCAGCTTCTGGCTTCAACATTAAAGACACCTATATACTAGTGG 1350

V R Q A P G K G L E W V A R I Y P T N G Y T R Y A
1351 GTGCGTCAGGCCCCGGTAAGGGCCTGGAATGGGTGCAAGGATTATCCTACGAATGGTTATACTAGATATGCC 1425

D S V K G R F T I S A D T S K N T A Y L Q M N S L
1426 GATAGCGTCAAGGGCCGTTTCACTATAAGCGCAGACACATCCAAAAACACAGCCTACCTGCAGATGAACAGCCTG 1500

R A E D T A V Y Y C S R W G G D G F Y A M D Y W G
1501 CGTGTGAGGACACTGCCGTCTATTATTGTTCTAGATGGGAGGGGACGGCTTCTATGCTATGGACTACTGGGT 1575

VH←|→Linker
Q G T L V T V S S A S T K G P S V G G G G S G G G
1576 CAAGGAACCTGGTCACCGTCTCCTCGCTAGCACCAAGGGCCCATCGGTGCGCGGTGGAGGCTCTGGTGGAGGC 1650

Linker←|→V_L
G S G G G G S D I Q M T Q S P S S L S A S V G D R
1651 GGTTCAGGAGCGGTGGATCTGACATCCAGATGACCCAGTCCCCGAGCTCCCTGTCCGCCTCTGTGGCGATAGG 1725

V T I T C R A S Q D V N T A V A W Y Q Q K P G K A
1726 GTTACCATCACCTGCCGTGCCAGTCAGGATGTGAATACTGCTGTAGCCTGGTATCAACAGAAACCAGGAAAAGCT 1800
P K L L I Y S A S F L Y S G V P S R F S G S R S G
1801 CCGAAACTACTGATTTACTCGGCATCCTTCCTCTACTCTGGAGTCCCTTCTCGCTTCTCTGGCTCCAGATCTGGG 1875
T D F T L T I S S L Q P E D F A T Y Y C Q Q H Y T
1876 ACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCGGAAGACTTCGCAACTTATTACTGTCAGCAACATTATACT 1950
T P P T F G Q G T K V E I K R Stop
1951 ACTCCTCCCACGTTCCGACAGGGTACCAAGGTGGAGATCAAACGTTGA 1998

Figure 37B

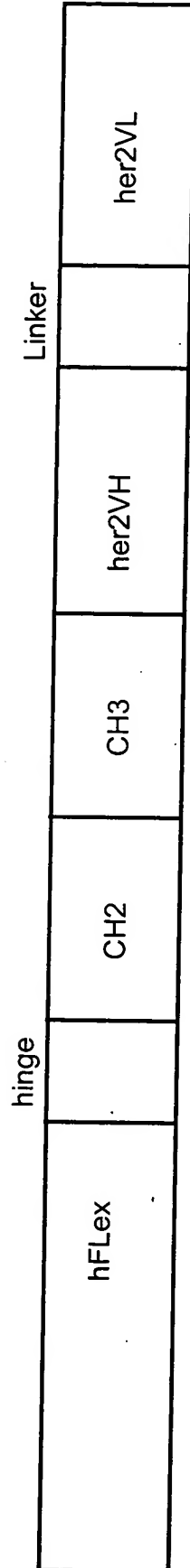


FIGURE 38

Figure 39

 |→SP
 M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACCTATCTCCTCTGCTGCTGCTGCTGAGCTCGGGA CT CAGT 0075

 SP←|→FLex
 G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGAC 0150

 Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

 L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGC 0300

 V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTCAACAAATGTGCCTTTAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC 0375

 N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCTCTGTCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

 S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGGTGCTGGAGCTGCACTGTGAGCCGACTCCTCAACCCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

 FLex←|→Linker Linker←|→Trailex
 A T A P T A P G G G G S G G G G S G G G G S V R E
0526 GCCACAGCCCCGACAGCCCCGGCGGTGGAGGCTCTGGTGGAGGCGGTTTCAGGAGGCGGTGGATCTGTGAGAGAA 0600

 R G P Q R V A A H I T G T R G R S N T L S S P N S
0601 AGAGGTCCTCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCAAACCTCC 0675

 K N E K A L G R K I N S W E S S R S G H S F L S N
0676 AAGATGAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCTTCCTGAGCAAC 0750

 L H L R N G E L V I H E K G F Y Y I Y S Q T Y F R
0751 TTGCACTTGAGGAATGGTGAAGTGGTCATGCATGAAAAAGGGTTTACTACATCTATTCCCAAACATACTTTCGA 0825

 F Q E E I K E N T K N D K Q M V Q Y I Y K Y T S Y
0826 TTTCAGGAGGAAATAAAGAAAAACAAAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTAT 0900

 P D P I L L M K S A R N S C W S K D A E Y G L Y S
0901 CCTGACCCTATATTGTTGATGAAAAGTGTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCC 0975

 I Y Q G G I F E L K E N D R I F V S V T N E H L I
0976 ATCTATCAAGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTGTCTGTAACAAATGAGCACTTGATA 1050

 D M D H E A S F F G A F L V G Stop
1051 GACATGGACCATGAAGCCAGTTTTTTTGGGGCCTTTTGTAGTTGGCTAA 1098

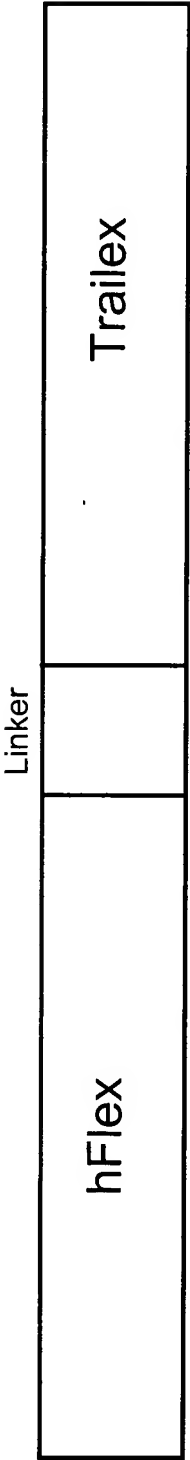


FIGURE 40

Figure 41

→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACACCTATCTCTCCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←→FLEX
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTGCTGGGTCCAAGATGCAAGGCTTGTCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTCAACAAATGTGCCTTTTCAGCCCCCCCCAGCTGTCTTCGCTTCCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGTGCCTGGAGTGCAGTGTGAGCCGACTCTCAACCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

FLEX←→Zipper
A T A P T A P M K Q I E D K I E E I L S K I Y H I
0526 GCCACAGCCCCGACAGCCCCGATGAAGCAGATCGAGGACAAAATTGAGGAAATCCTGTCCAAGATTACCACATC 0600

Zipper←→Trailex
E N E I A R I K K L I G E T S E E T I S T V Q E K
0601 GAGAACGAGATCGCCCGGATTAAGAAACTATTGGCGAGACCTCTGAGGAAACCATTTCTACAGTTCAAGAAAAG 0675

Q Q N I S P L V R E R G P Q R V A A H I T G T R G
0676 CAACAAAATATTTCTCCCTAGTGAGAGAAAGAGGTCTCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGA 0750

R S N T L S S P N S K N E K A L G R K I N S W E S
0751 AGAAGCAACACATTGTCTTCTCAAACCTCAAGAATGAAAGGCTCTGGCCGCAAAATAAACTCCTGGGAATCA 0825

S R S G H S F L S N L H L R N G E L V I H E K G F
0826 TCAAGGAGTGGGCATTCTCTGAGCAACTTGACATTGAGGAATGGTGAAGTGGTCATCCATGAAAAAGGGTTT 0900

Y Y I Y S Q T Y F R F Q E E I K E N T K N D K Q M
0901 TACTACATCTATTCCAAACATCTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGACAAACAAATG 0975

V Q Y I Y K Y T S Y P D P I L L M K S A R N S C W
0976 GTCCAATATATTACAAATACACAAGTTATCTGACCCTATATTGTGTGATGAAAAGTGCTAGAAATAGTTGTTGG 1050

S K D A E Y G L Y S I Y Q G G I F E L K E N D R I
1051 TCTAAAGATGCAGAATATGGACTCTATTCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAATGACAGAATT 1125

F V S V T N E H L I D M D H E A S F F G A F L V G
1126 TTTGTTTCTGTAACAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTTGGGGCCTTTTGTAGTTGGC 1200

STOP
1201 TAA

1203

Figure 42

|→SP
M T V L A P A W S P T T Y L L L L L L L S S G L S
0001 ATGACAGTGTGGCGCCAGCCTGGAGCCCAACACCTATCTCTCTGCTGCTGCTGCTGAGCTCGGGACTCAGT 0075

SP←|→Flex
G T Q D C S F Q H S P I S S D F A V K I R E L S D
0076 GGGACCCAGGACTGCTCCTTCCAAACACAGCCCATCTCTCCGACTTCGCTGTCAAATCCGTGAGCTGCTCTGAC 0150

Y L L Q D Y P V T V A S N L Q D E E L C G G L W R
0151 TACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTCGGGGGCCTCTGGCGG 0225

L V L A Q R W M E R L K T V A G S K M Q G L L E R
0226 CTGGTCTGGCAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGTCTGGAGCGC 0300

V N T E I H F V T K C A F Q P P P S C L R F V Q T
0301 GTGAACACGGAGATACACTTTGTACCAAAATGTGCCTTTTCAGCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC 0375

N I S R L L Q E T S E Q L V A L K P W I T R Q N F
0376 AACATCTCCCGCTCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTC 0450

S R C L E L Q C Q P D S S T L P P P W S P R P L E
0451 TCCCGGTGCTGGAGCTGCAGTGTCAAGCCGACTCCTCAACCTGCCACCCCATGGAGTCCCGGGCCCTGGAG 0525

Flex←|→hinge hinge←|→CH2
A T A P T A P E P K S C D K T H T C P P C P A P E
0526 GCCACAGCCCCGACAGCCCCGGAGCCCAATCTTGTGACAAAACCTACACATGCCACCGTGGCCAGCAGCTGAA 0600

L L G G P S V F L F P P K P K D T L M I S R T P E
0601 CTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGACCCCTGAG 0675

V T C V V V D V S H E D P E V K F N W Y V D G V E
0676 GTCACATGCGTGGTGGTGGAGCTGAGCCACGAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAG 0750

V H N A K T K P R E E Q Y N S T Y R V V S V L T V
0751 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTAACGGGTGGTCTGCGTCTCACCCTC 0825

L H Q D W L N G K E Y K C K V S N K A L P A P I E
0826 CTGACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAG 0900

CH2←|→CH3
K T I S K A K G Q P R E P Q V Y T L P P S R D E L
0901 AAAACATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACCCCTGCCCCATCCCGGGATGAGCTG 0975

T K N Q V S L T C L V K G F Y P S D I A V E W E S
0976 ACCAAGAACCAGGTGAGCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGC 1050

N G Q P E N N Y K T T P P V L D S D G S F F L Y S
1051 AATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGTGACTCCGACGGCTCCTTCTCTCTACAGC 1125

K L T V D K S R W Q Q G N V F S C S V M H E A L H
1126 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 1200

CH3←|→Trailex
N H Y T Q K S L S L S P G K V R E R G P Q R V A A
1201 AACCACTACAGCAGAAGAGCCTCTCCCTGTCTCCCGTAAAGTGAGAGAAAGAGGTCTCAGAGAGTAGCAGCT 1275

H I T G T R G R S N T L S S P N S K N E K A L G R
1276 CACATAACTGGGACCAGAGGAAGAAGCAACATTGTCTTCTCCAACTCCAAGAATGAAAAGGCTCTGGGCCG 1350

K I N S W E S S R S G H S F L S N L H L R N G E L
1351 AAAATAAATCTCTGGGAATCATCAAGGAGTGGGCATTCTTCTGAGCAACTTGCACITGAGGAATGGTGAAGCTG 1425

V I H E K G F Y Y I Y S Q T Y F R F Q E E I K E N
1426 GTCATCCATGAAAAGGGTTTACTACATCTATTCCCAACATACTTTTGATTTTCAGGAGGAAATAAAAGAAAC 1500

T K N D K Q M V Q Y I Y K Y T S Y P D P I L L M K
1501 ACAAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTATCTGACCCTATATTGTTGATGAAA 1575

S A R N S C W S K D A E Y G L Y S I Y Q G G I F E
1576 AGTGCTAGAAATAGTTGTGTGCTAAAGATGCAGAAATGGAAGCTTATTCATCTATCAAGGGGAATATTTGAG 1650

L K E N D R I F V S V T N E H L I D M D H E A S F
1651 CTTAAGGAAATGACAGAATTTTGTCTGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCAGTTT 1725

F G A F L V G SIOP
1726 TTGGGGCCITTTTAGTTGGCTAA 1749

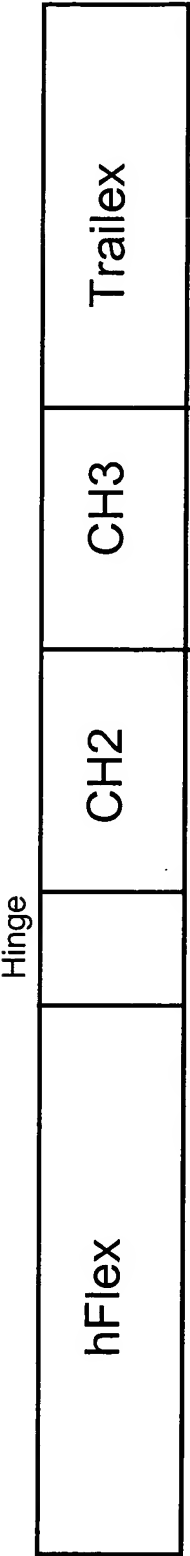


FIGURE 43

Figure 44

	HGFs+					
	-	SCF	G-CSF	GM-CSF	IL-3	CSF-1
-	1	2	33	20	12	1
FL	2	22	52	65	52	12
chSM	0	3	29	22	10	0
huSM	0	2	25	26	14	1
chSM/FL	5	23	59	75	46	12
huSM/FL	3	25	56	70	50	14

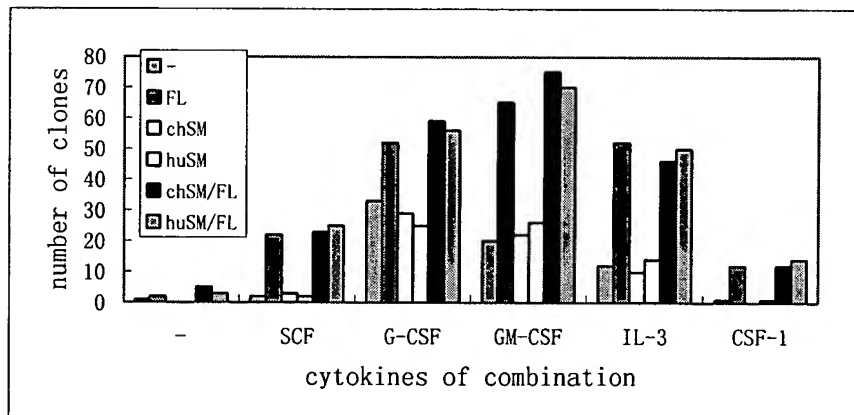
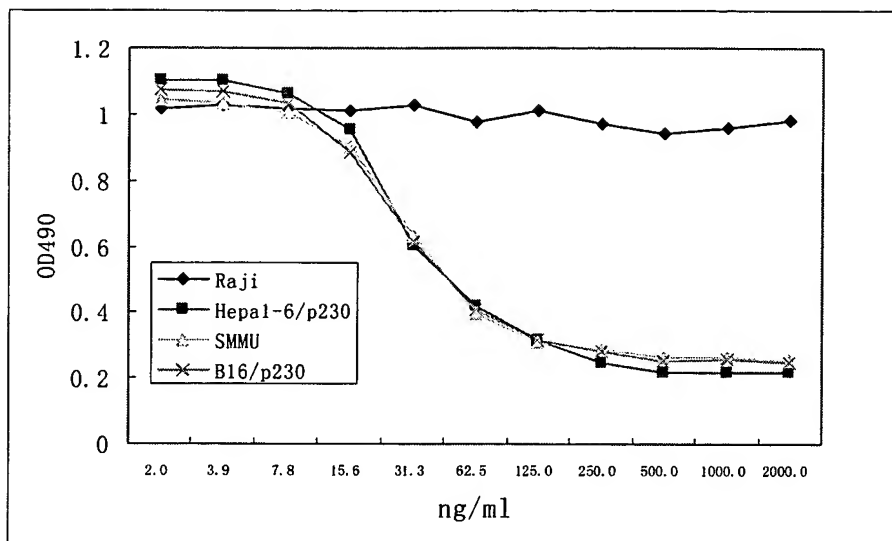


Figure 45

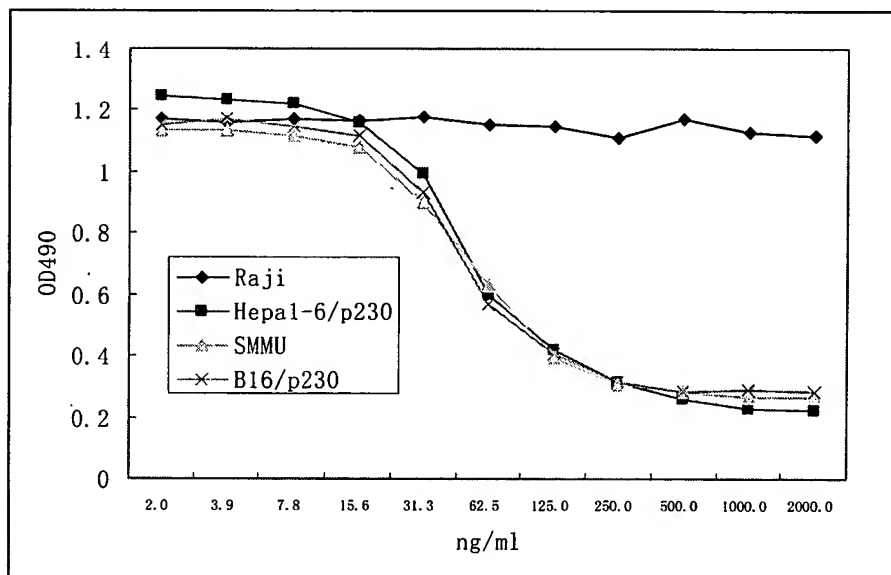
Item	CD3 ⁺ NK1.1 ⁺ (NK) ($\times 10^6$)			CD3 ⁺ NK1.1 ⁺ (T) ($\times 10^6$)			CD3 ⁺ NK1.1 ⁺ (NK) ($\times 10^6$)			CD11c ⁺ (DC) ($\times 10^6$)		
	FL	chSM/FL	huSM/FL	FL	chSM/FL	huSM/FL	FL	chSM/FL	huSM/FL	FL	chSM/FL	huSM/FL
spleen	0	2.0	3.0	3.5	40	38	40	7.0	6.0	6.5	3.0	2.8
	3	3.0	4.0	4.0	50	55	53	5.0	9.0	10.0	5.0	8.5
	6	6.0	5.0	5.5	76	81	82	11	18.0	18.5	35	55
	8	16	15	14	68	72	70	21	28	30	85	133
	10	17	21	23	75	80	83	17	32	31	180	182
	12	24	29	30	50	53	55	50	49	47	190	165
	15	20	18	17	38	39	40	27	33	35	180	161
	18	9	12	10	22	26	28	41	49	51	150	109
liver	0	1.0	1.0	0.9	1.0	1.3	1.1	5.0	4.5	4.8	2.0	3.5
	3	2.0	3.0	3.5	1.5	1.8	2.0	6.0	6.9	7.0	3.0	4.3
	6	3.0	5.0	4.5	1.5	1.8	1.9	5.0	4.5	4.8	5.0	5.9
	8	13.0	12.0	11.0	1.5	1.9	2.1	9.0	9.9	9.5	5.5	3.7
	10	20	18.0	19.0	3.8	3.5	3.8	3.0	2.8	3.0	18.5	16.9
	12	11	17.0	16.0	5.6	5.5	5.2	19	19	20	9.0	10.1
	15	5.0	6.0	6.5	3.0	2.8	3.0	9.0	8.0	7.5	2.5	5.1
	18	2.0	3.0	3.0	3.0	3.4	3.5	2.0	2.0	2.3	8.0	7.0
Bone marrow	0	2.0	1.0	1.5	2.0	2.0	2.5	1.0	1.0	1.2	2.0	2.0
	3	1.0	2.0	2.0	5.9	5.5	5.3	1.8	1.2	1.1	3.0	1.9
	6	1.5	1.8	2.0	1.9	1.8	1.8	1.8	1.2	1.3	15.0	11.5
	8	4.0	4.5	5.0	1.5	1.5	1.8	2.5	1.9	2.1	20	33
	10	4.0	5.0	4.5	2.5	1.9	2.1	2.0	1.9	2.0	39	36
	12	4.0	5.2	5.5	2.5	1.5	1.6	5.0	5.7	6.1	29	31
	15	4.0	4.0	4.5	3.9	3.4	3.5	5.0	4.2	4.5	19	15
	18	3.0	3.3	3.5	1.9	1.8	2.0	4.0	3.7	3.4	14	13

Figure 46A



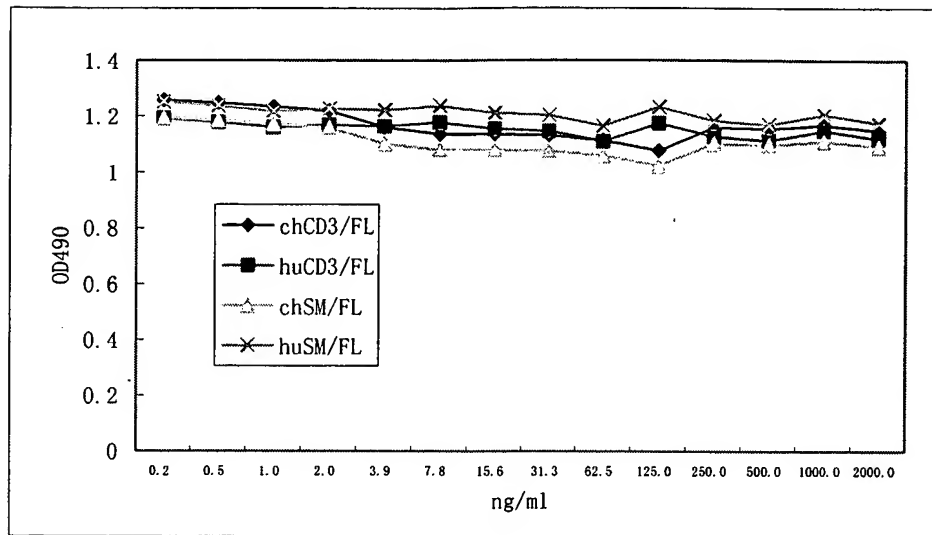
chSM5-1

Figure 46B



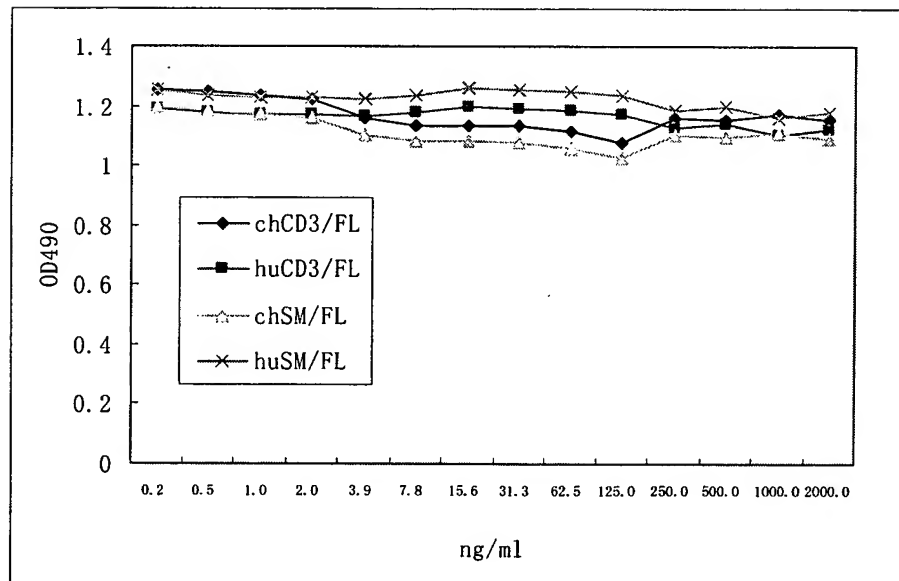
huSM5-1

Figure 47A



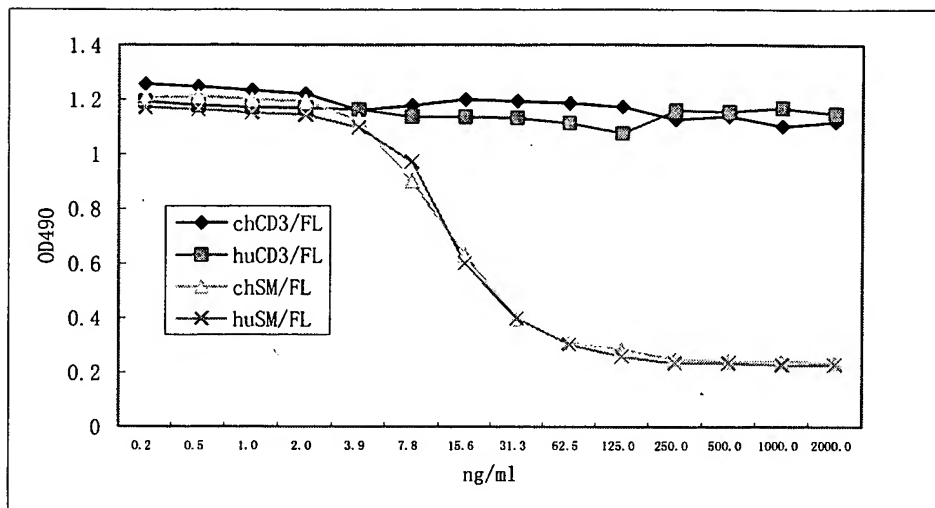
B16

Figure 47B



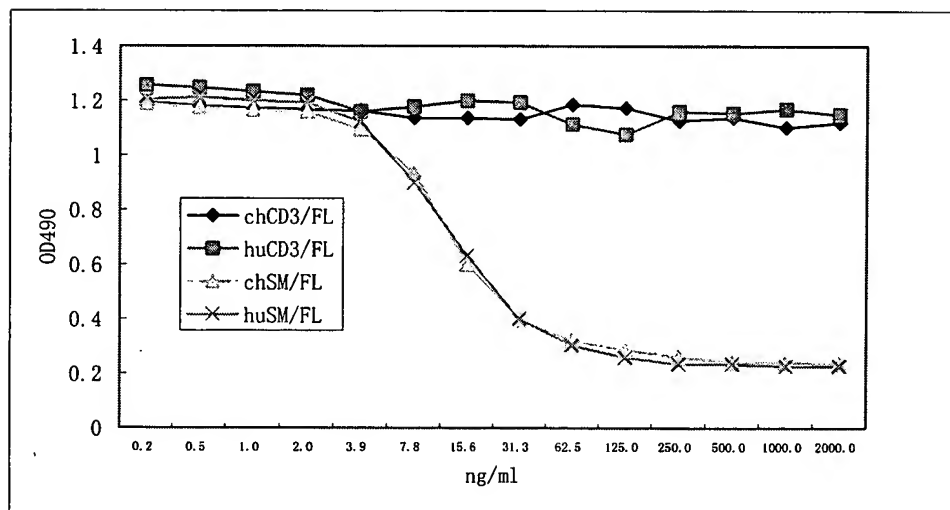
hep1-6

Figure 47C



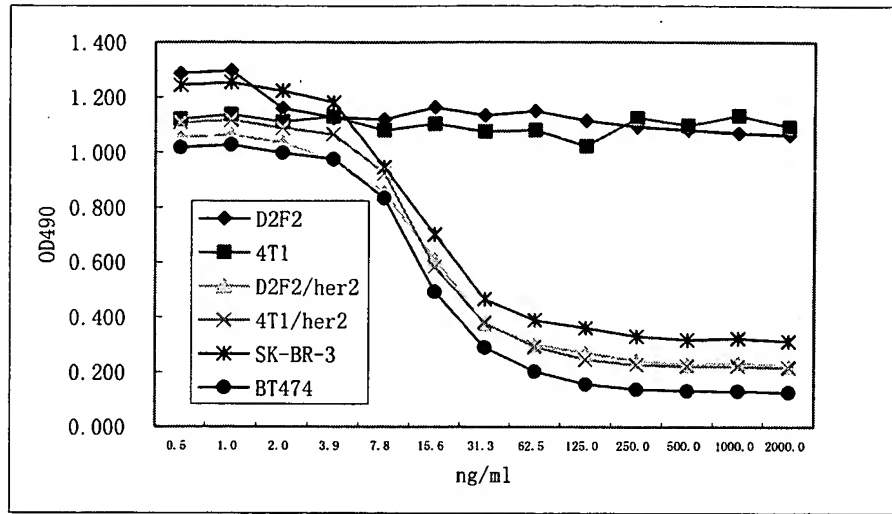
B16/p230

Figure 47D



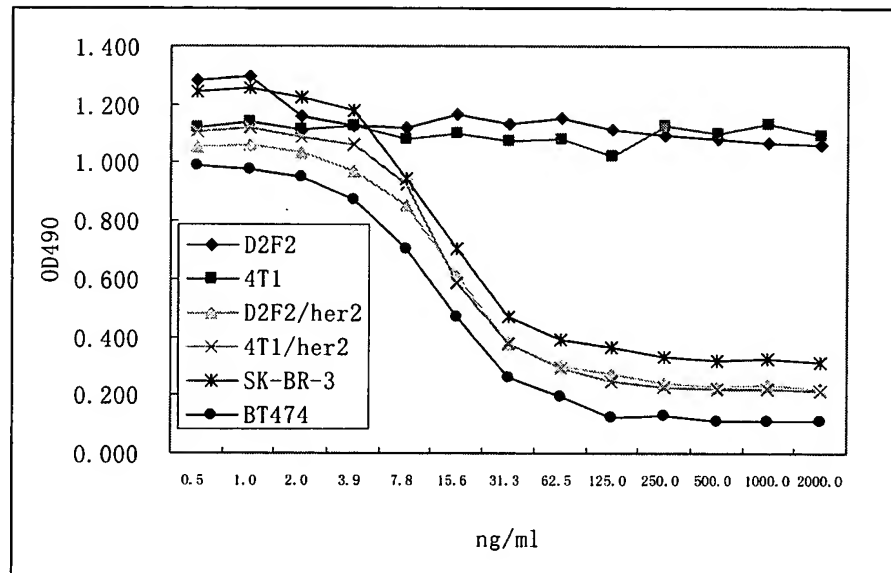
hep1-6/p230

Figure 48A

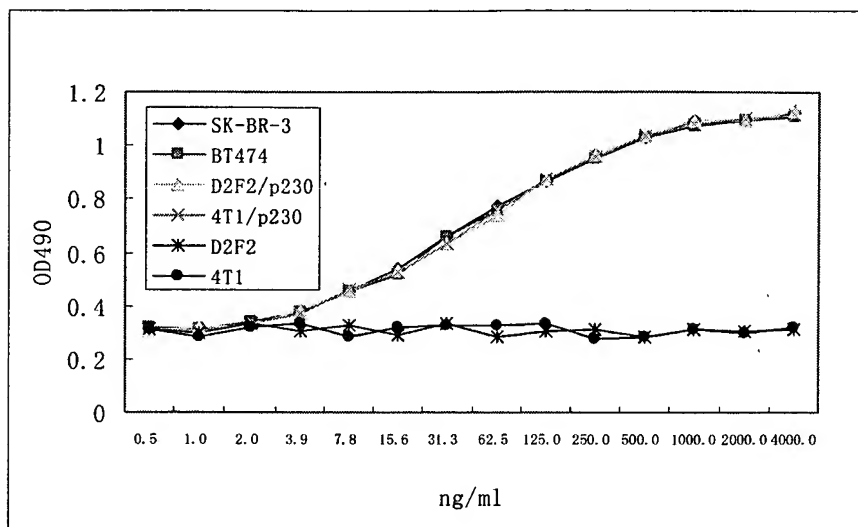


FL/her2

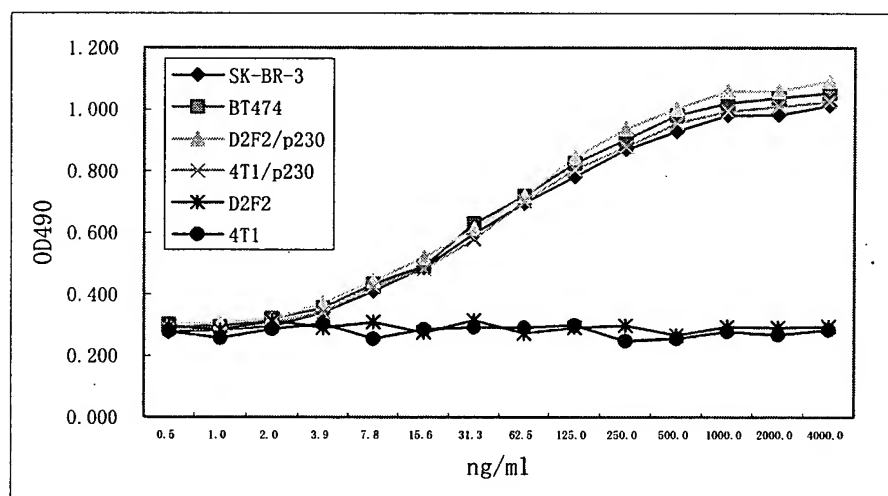
Figure 48B



herceptin

Figure 49A

her2/FL

Figure 49B

herceptin

Figure 50

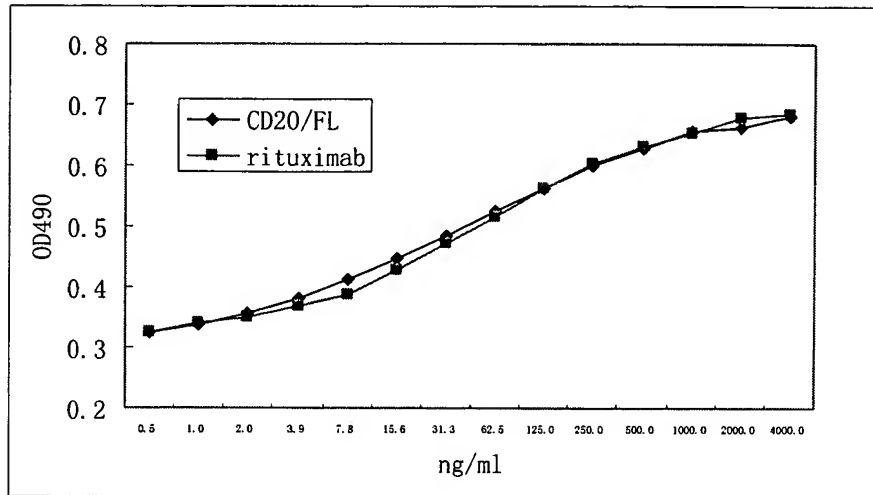
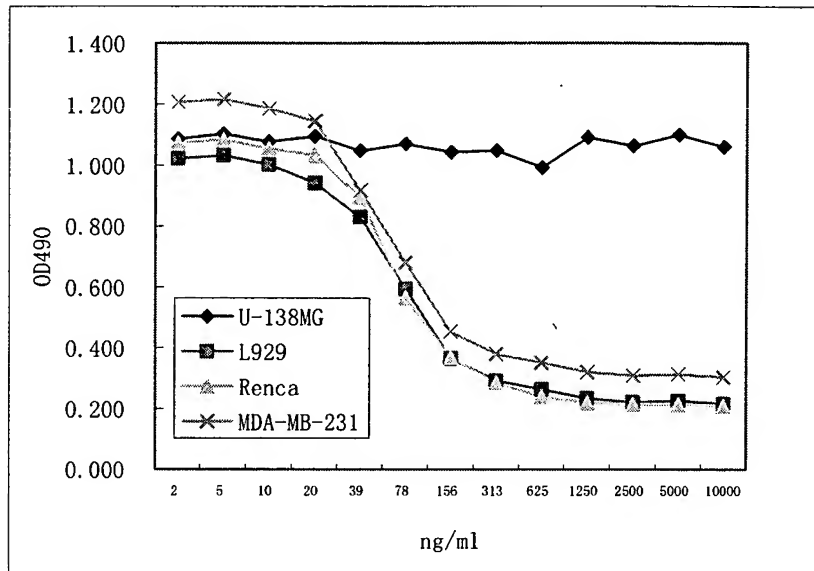
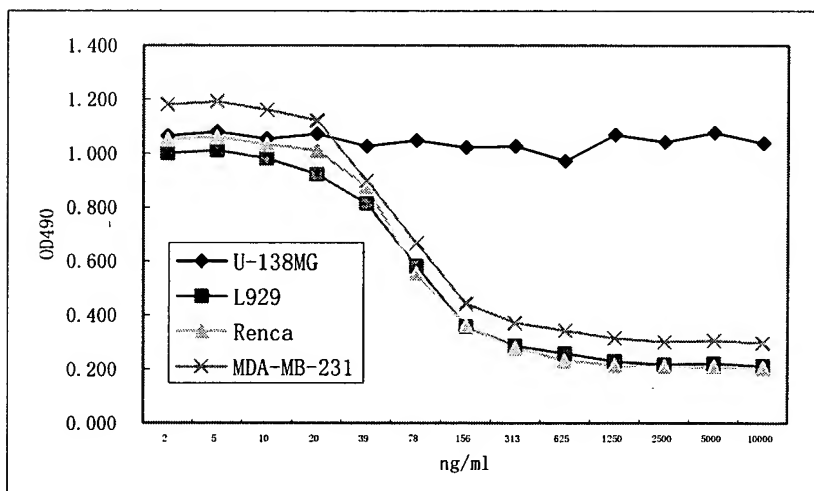


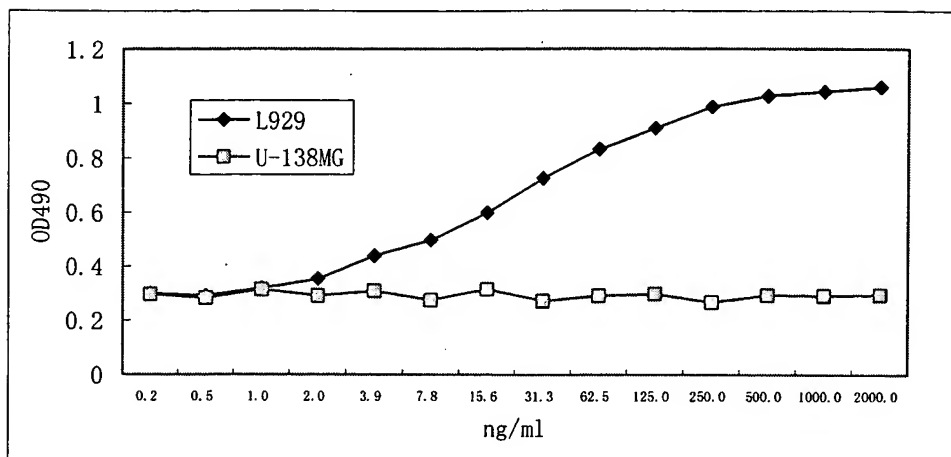
Figure 51A

Trail/FL

Figure 51B

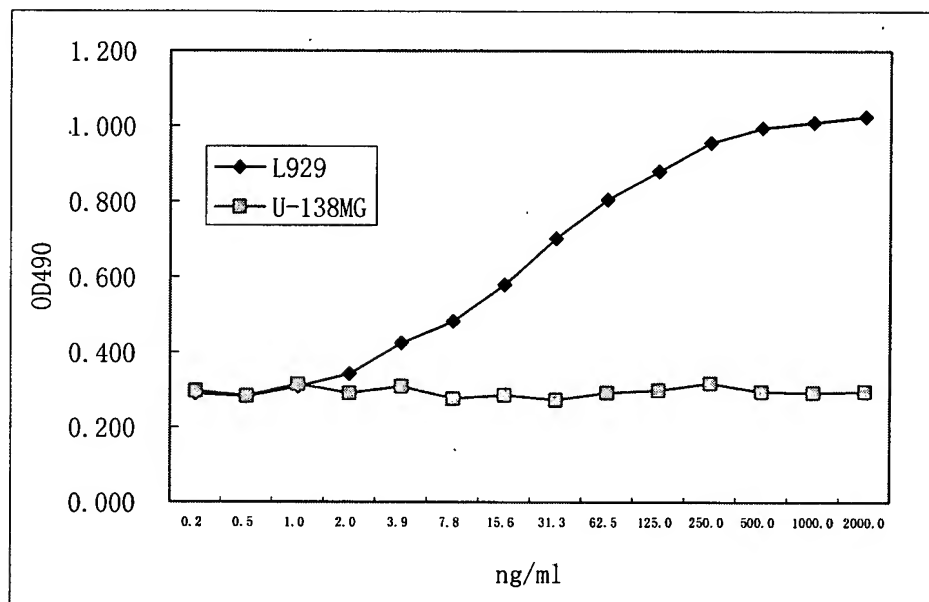
Trail

Figure 52A



Trail/FL

Figure 52B



Trail

Figure 53

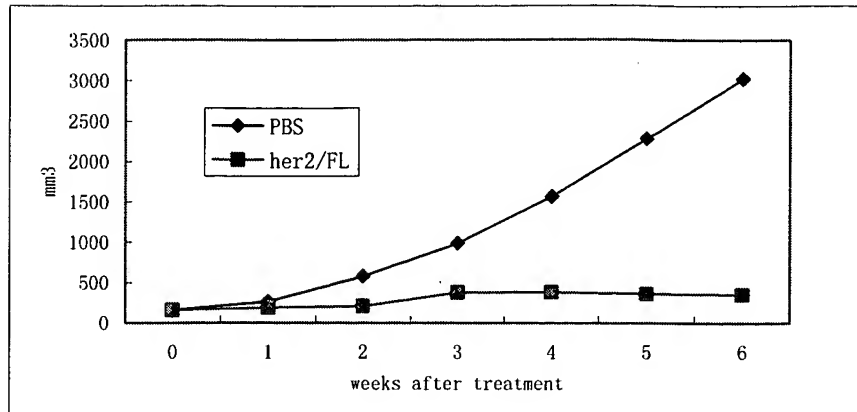


Figure 54

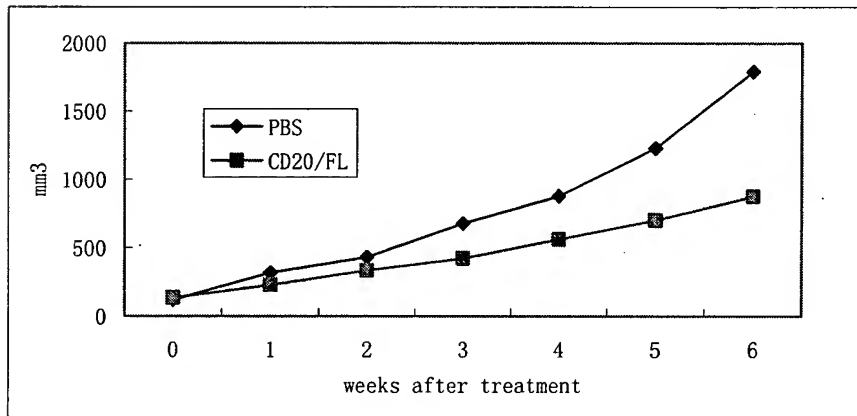
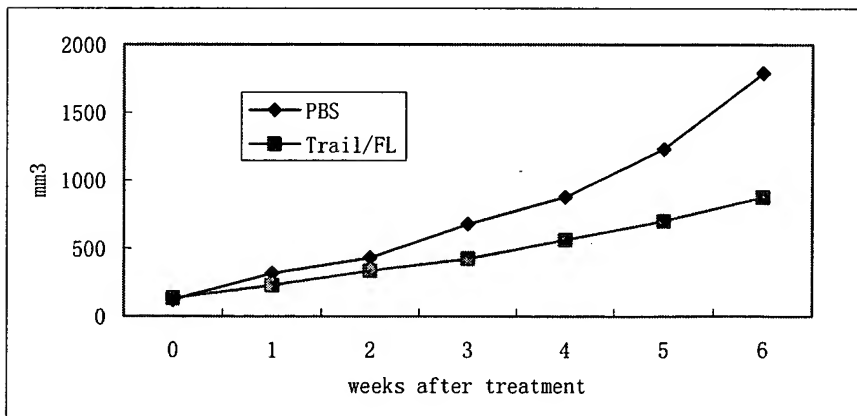


Figure 55



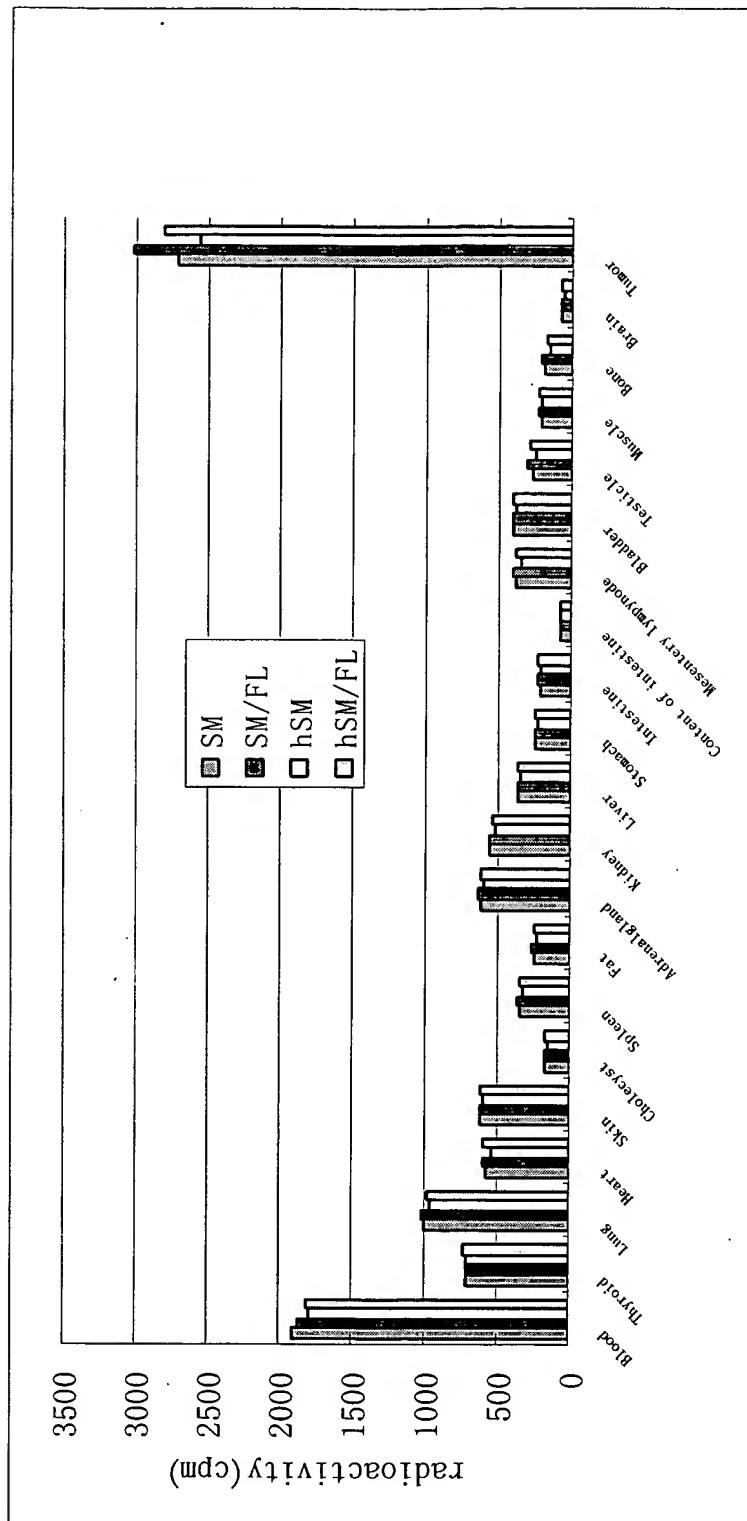


FIGURE 56

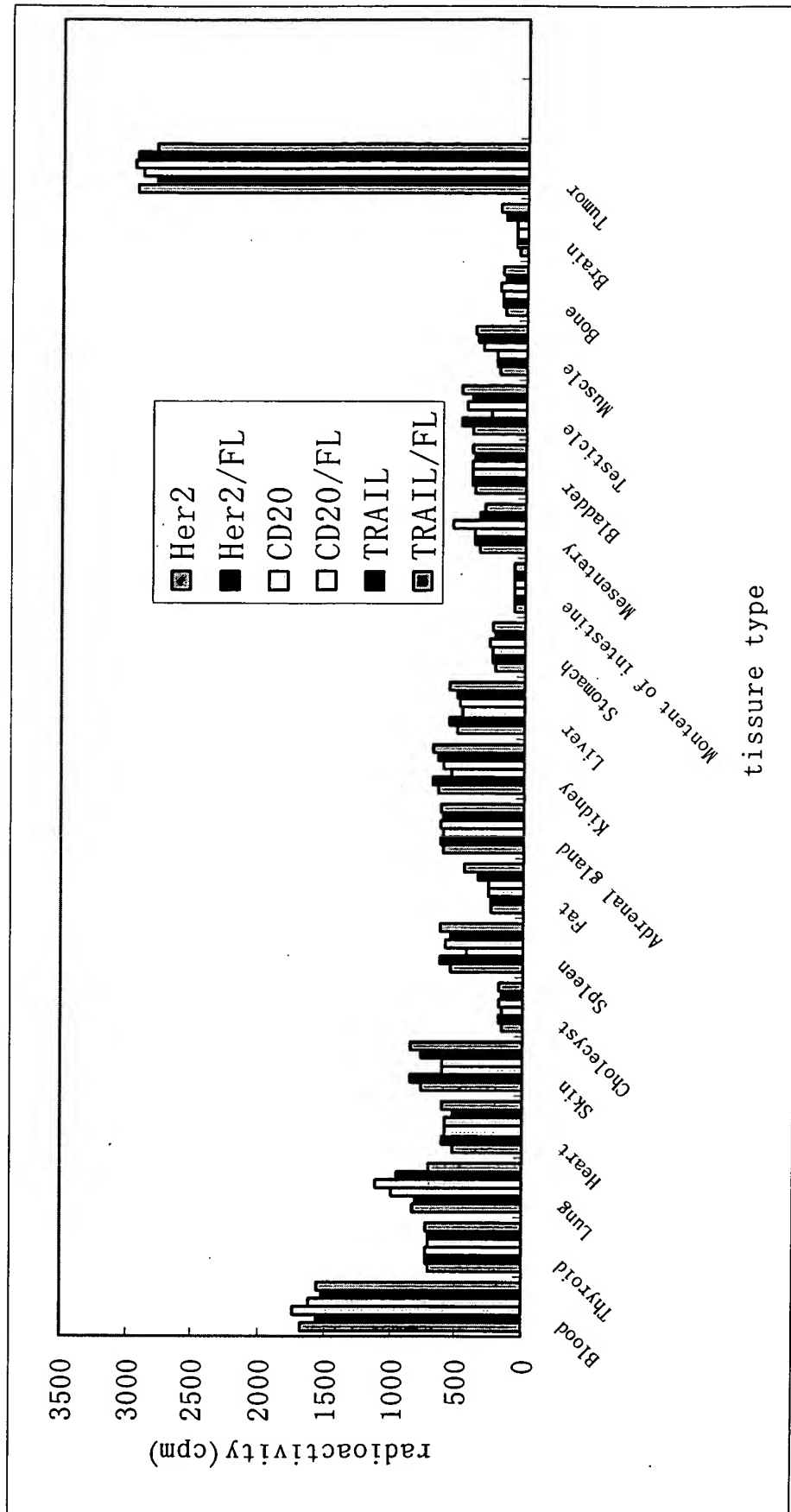


FIGURE 57